

OM protein - protein search, using sw model
 copyright (c) 1993 - 2004 Compugen Ltd.

Title: US-09-780-576-2
 Perfect score: 1778
 Sequence: 1 MQAVDNLTSAPGNTSLTRD.....SQDNRKKEODGGDPNEEPM 342
 Run on: February 4, 2004, 14:18:01 ; Search time 21 Seconds
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 328717 seqs, 42310858 residues
 Total number of hits satisfying chosen parameters: 328717
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Result No.	Score	Query	Match Length	DB ID	Description
1	1778	100.0	342	3 US-08-652-824-2	Sequence 2, Appli
2	823	46.3	333	3 US-09-221-456-2	Sequence 2, Appli
3	823	46.3	333	4 US-09-558-740-2	Sequence 2, Appli
4	797	44.8	333	2 US-08-112-871-1	Sequence 1, Appli
5	772	43.4	325	2 US-08-667-948A-29	Sequence 29, Appli
6	772	43.4	325	3 US-08-667-947A-29	Sequence 29, Appli
7	772	43.4	338	3 US-08-988-876-8	Sequence 8, Appli
8	772	43.4	338	3 US-09-303-54A-2	Sequence 2, Appli
9	679.5	38.2	358	3 US-08-888-876-3	Sequence 3, Appli
10	546.5	30.7	293	2 US-08-467-948A-6	Sequence 6, Appli
11	546.5	30.7	293	3 US-08-467-947A-6	Sequence 6, Appli
12	27.4	488	27	1 US-08-023-344-28	Sequence 28, Appli
13	410.5	23.1	326	1 US-08-118-270-39	Sequence 39, Appli
14	410.5	23.1	326	5 PCT-US91-08528-39	Sequence 39, Appli
15	392.5	22.1	342	3 US-08-988-876-9	Sequence 9, Appli
16	379.5	21.3	361	1 US-08-333-750-4	Sequence 4, Appli
17	379.5	21.3	361	3 US-08-352-678-4	Sequence 4, Appli
18	379.5	21.3	361	4 US-08-556-954-4	Sequence 4, Appli
19	379.5	21.3	361	4 US-09-170-456D-7B	Sequence 78, Appli
20	379.5	21.3	361	4 US-09-170-496D-206	Sequence 206, Appli
21	379.5	21.3	361	5 PCT-US91-09656-4	Sequence 4, Appli
22	378	21.3	316	4 US-09-690-455-69	Sequence 69, Appli
23	376	21.1	381	3 US-08-852-824-17	Sequence 17, Appli
24	374.5	21.1	381	1 US-08-467-125-2	Sequence 2, Appli
25	374.5	21.1	381	2 US-08-911-320A-1	Sequence 2, Appli
26	374.5	21.1	381	3 US-08-101-102-3	Sequence 2, Appli
27	349.5	19.7	302	2 US-08-467-948A-30	Sequence 30, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENT

Copyright (c) 1993 - 2004 Compugen Ltd.
 GenCore version 5.1.6
 Run on: February 4, 2004, 14:18:01 ; Search time 21 Seconds
 (without alignments)
 689.063 Million cell updates/sec
 OM protein - protein search, using sw model
 Title: US-09-780-576-2
 Perfect score: 1778
 Sequence: 1 MQAVDNLITSAPGNTSLTRD.SDQNRKEEQDGDDPNEETPM 342
 Scoring table: BLOSUM62
 Gapov 10.0 , Gapext 0.5

28	349.5	19.7	302	3	US-08-467-94A-30
29	347.5	19.5	346	4	US-09-55-876-2
30	339	19.1	344	2	US-08-467-94B-A-8
31	339	19.1	344	3	US-08-467-94A-B
32	337	19.0	68	3	US-08-905-223-327
33	32.5	18.7	339	4	US-09-170-496D-182
34	329.5	18.5	339	1	US-08-153-648-44
35	329.5	18.5	32	2	US-08-812-871-3
36	329.5	18.5	339	3	US-09-293-843A-44
37	329.5	18.5	339	4	US-09-088-337B-B-44
38	329.5	18.5	339	4	US-09-170-496D-32
39	329.5	18.5	339	5	PCT-US93-11153-44
40	329.5	18.5	339	5	PCT-US93-01180-2
41	329	18.5	359	1	US-08-041-219A-6
42	329	18.5	359	1	US-08-417-122-B-6
43	327.5	18.4	395	1	US-08-97-918-2
44	327.5	18.4	395	1	US-08-476-000-2
45	327.5	18.4	395	1	US-08-472-840-2

Patent No. 6162899
 GENERAL INFORMATION:
 APPLICANT: SATHE, GANESH
 APPLICANT: HAUSER, WENDY
 APPLICANT: MUIR, ALISON
 APPLICANT: CHAMBERS, JON
 APPLICANT: SZERKES, PHILIP
 TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND ANTAGONISTS OF THE HNEAA81 RECEPTOR
 NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ratner & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PassEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/221,456
 FILING DATE: 28-DEC-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/956,975
 FILING DATE: 23-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F.
 REGISTRATION NUMBER: 22,031
 REFERENCE/DOCKET NUMBER: GH-70318-1
 TELEPHONE: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 / CHARACTERISTICS:
 LENGTH: 333 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-221-456-2

Query Match 46.3%; Score 823; DB 3; Length 333;
 Best Local Similarity 49.7%; Pred. No. 7,6e-63; Indels 2; Gaps 1;
 Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

Qy 17 CTRDYKITQVLPFLIYTCVQTSVITYFMYISIPLGLITIDRQKTRPFTNSPK 136
 Db 15 CPDRTRIVQVFPALTYVFLGILNLTLALWVEHIPSSTIYIURNTLVADLIMLM 74

Qy 77 FPKILSDAKLGIGPLRTFCVQTSVITYFMYISIPLGLITIDRQKTRPFTNSPK 136
 Db 75 LPFKILSDSHLAPMQLRAFVCPRESSVITYMVGIVLGLIAFDRLTKIRPLNIFLK 134

Qy 137 NLGAKILSVVIAFMFLISLPMLNTQPRDKNVKCSFLKSEPGLVMBIVNYICQV 196
 Db 135 KPVFAKTVS1FWFLFFISLPNTLSNEATPSVKKCASKLGPGLKWHOMNNICQF 194

Qy 197 IFWINFLIVCVCTYLTKELIYRSVTRGVGYPRKVKVNPFLAYPIFVPPPHAR 256
 Db 195 IPWTYFILMLVYYVIAKYDSRKSKDKRNKLEGKVYFVVVAVFVCFAPPFIFAR 254

Qy 257 IPTYLSQTRDVFDCTAENTLYKESTIWLTSINAUCDPEYFLCKSFASRSLISMKCP 316
 Db 255 VPYTHSQTNKTCDRLQQLTAKETTLFLAATNCNDPLYIFLCKTPTEKLPCMQ-G 312

Qy 317 NSATSLSQDNRKKEQD 332
 Db 313 RKTASSQENHSSQFD 328

RESULT 4
 US-09-812-871-1
 Sequence 1, Application US/08/12871
 Patent No. 5955303
 GENERAL INFORMATION:
 APPLICANT: All-Young, Janice
 APPLICANT: Gieger, Karl
 APPLICANT: MuZong, Cheng
 TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR LIKE PROTEIN
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto

STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/812,871
 FILING DATE: Filed Herewith
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0237 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 333 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: MMLRD01
 CLONE: 568987
 US-08-812-871-1

Query Match Score 797; DB 2; Length 333;
 Best Local Similarity 47.8%; Pred. No. 1.3e-61;
 Matches 151; Conservative 57; Mismatches 106; Indels 2; Gaps 1;

Db 17 CTRDYKITQVLPPLLYLTFPGLTNGLMRPFQIRSKSNPFIPLKNTYISDLMILIT 76
 Qy 77 FPKKILSDAKLGPGPLRFVCPQVTSVIFYFTMVISISFLGLTIDSYQKTRPFITSNPK 136
 Db 75 LPPKILSDSHLAPWQLRAFPVCFESSSVIYETMYGIVLGLIAFDRFLKIRPLNIFLK 134
 Qy 137 NLIGAKLSSVVVIAWFMLLSLPMILTNRPPDKNYTKCSFKLSEFGLYWHEIVNYICQV 196
 Db 135 KPYFAKTVSIFWFLFLFISLPMILSNKEATPSSVKCASJXGPGLKRNHQMVANNICQF 194
 Qy 197 IFWFINLLIVCYTLLKELYRSYVRTRGVGKVRKVNVKVFLIAVFFFCYVPPFHAR 256
 Db 195 IFWTLVIMLFVTVIARKVDSYRKSKCKDRNNKRLLEGKVFVVFVCFAPPFHAR 254
 Qy 257 IPIYTLSPQRDFVFACTENLFLYKESTLWITSLNACLDPFIYFLCKSFNSLJSMIKCP 316
 Db 255 VPTPHSQTPNNKTKCRLQNLQFLAKETTLFLAATNCMDPLISIFLCKKFTERKLPCHQ--G 312
 Qy 317 NSATSLSQDNRKKEQD 332
 Db 313 RKTASSQENHSSGTD 328

RESULT 5
 US-08-467-948A-29
 Sequence 29, Application US/08467948A
 Patent No. 598164
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.

APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 TITLE OF INVENTION: Coupled Receptor GPR2
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 29:
 SUBSEQUENCE CHARACTERISTICS:
 LENGTH: 325 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-467-948A-29

Query Match Score 772; DB 2; Length 325;
 Best Local Similarity 47.5%; Pred. No. 1.7e-59;
 Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;
 Db 2 NSTRTQQPPEESQNLLITQIIPVLYCMVFTAGILNGSWSWIFTYVPSRSKSPFVYLN 61
 Qy 6 NLTSAGNTNSLICRDYKITQVLFLPLXYLVLEPGVLTINGLAMRIFFQIRSKSNPFIPLKLN 65
 Db 2 NSTRTQQPPEESQNLLITQIIPVLYCMVFTAGILNGSWSWIFTYVPSRSKSPFVYLN 61
 Qy 66 TVSDLMILITPFPKLSDAKLGPGPLRTFVQVTSVIFYFTMVISISFLGLTIDSYQK 125
 Db 62 IVDADFSNLTFPKLGDSGLGPWQLNVPFRVSAVLFYVNMVY51VFEGLISDFRYK 121
 Qy 126 TTRPEKTSMPKNLGAIIISVWAFMELLSLPMILTNRPPDKNYTKCSFKLSEFGLYV 185
 Db 122 IVKPLWTSFQTSYSKLSLIVWMLLAPNLLIQNSREVQIKCIELKSEIGRK 181
 Qy 186 WHEIVNYICQVIFWIFNFLIIVCYTLLKELYRSYVRTRGVGKVRKVNVKVFLIAVFF 245
 Db 182 WHKASNYFVAIFWIFLILIFYTAITKIFKSHIKSSRNSTSVKKKSRNIFSVWPV 241
 Qy 246 FICYPFFIFARIPTYLSQTDYEDCTAENTLFLYKESTLWITSLNACLDPFIYFLCKSF 305
 Db 242 FVCVPYHARIPTKSCTEAHYSCQSKETURYMKEFTLLUSAANYCLDPIYFLCQF 301
 Qy 306 RNLSLSMLKCPNSA 319
 Db 302 RETLICKDHPIPLKA 315

RESULT 6
 US-08-467-947A-29
 Sequence 29, Application US/08467947A
 Patent No. 6090515
 GENERAL INFORMATION:

APPLICANT: LI, YI
 APPLICANT: CAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BUILT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Coupled Receptor GPR1
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 110 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENT RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,947A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFF, ERIC K.
 REGISTRATION NUMBER: 36,688
 TELEPHONE: 202-371-2540
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 325 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-467-947A-29

Query Match 43 4%; Score 772; DB 3; Length 325;
 Best Local Similarity 47.5%; Pred. No. 17e 58; Mismatches 105; Indels 0; Gaps 0;
 Matches 149; Conservative 60; Clones: 285955
 US-08-467-947A-29

Qy 6 NLTSAQNTSLCSTDYKITQQLFPLIYTLYFVGLITNLGAMRIFFOIRSKNSNFIIFLKN 65
 Db 2 NSTSTQPDBCSQNLLITQIQIPVLYCMVTEAGILLNGSVWIFFYVSSKSFYIKN 61
 Qy 66 TVISDLMILTPPKFLSDAQLGTGPRLTFCQTSVITYFTMYKISIISFGLITIDRYK 125
 Db 62 IIVIADEPMISLTPPKFLGDSCGPQNLAVFCRVSAVLFVNMYVSIVEGLISFDRYK 121
 Qy 126 TTRPFKTSNPKNLGAKILSIVIWAQMLLISLSPNMLTNEQPRDKNVKCSFLSBFGLV 185
 Db 122 IVKPLWISFIQSYSYSKLISLIVWMLLIAVPNLTQNSVRETOQKCIELSELGRK 181
 Qy 186 WHBIVNYTCOVIFWINFLIVTCYTLIKEIYRSTVRTRGVKGVPKCKVNVKFIIAYF 245
 Db 182 WHKASNYTFVAFWVIFLLIVFYTATKKFKSHLKSSNNSTSVKKSRRNIFIVVF 241
 Qy 246 FIGCFPFFPARITYTLESDTYDFDCTAENTLYVKESTLMTSINAQCLDPFTLCKSF 305
 Db 242 FVCFVPTHARIYFTKSGQTEAHYSCQSKEIILRYMKBFTLSSAANVCLDPIYFFLQCFF 301
 Qy 306 RNSLISMKCPNSA 319
 Db 302 REILCKKUHPLKA 315

RESULT 7
 US-08-988-876-8
 Sequence 8, Application US/0898876
 Patent No. 6063516
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED WITH IMMUNE RESPONSE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTEQ FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: FF-0441 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-955-0555
 TELEX: 650-845-4166
 LIBRARY: GenBank
 CLONE: 285955
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 338 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 IMMEDIATE SOURCE:
 US-08-988-876-8

Query Match 43 4%; Score 772; DB 3; Length 338;
 Best Local Similarity 47.5%; Pred. No. 1.7e 58; Mismatches 105; Indels 0; Gaps 0;
 Matches 149; Conservative 60; Clones: 285955
 Qy 6 NLTSAQNTSLCSTDYKITQQLFPLIYTLYFVGLITNLGAMRIFFOIRSKNSNFIIFLKN 65
 Db 3 NSTSTQPDBCSQNLLITQIQIPVLYCMVTEAGILLNGSVWIFFYVSSKSFYIKN 61
 Qy 66 TVISDLMILTPPKFLSDAQLGTGPRLTFCQTSVITYFTMYKISIISFGLITIDRYK 125
 Db 63 IIVIADEPMISLTPPKFLGDSCGPQNLAVFCRVSAVLFVNMYVSIVEGLISFDRYK 122
 Qy 126 TTRPFKTSNPKNLGAKILSIVIWAQMLLISLSPNMLTNEQPRDKNVKCSFLSBFGLV 185
 Db 123 IVKPLWISFIQSYSYSKLISLIVWMLLIAVPNLTQNSVRETOQKCIELSELGRK 181
 Qy 186 WHBIVNYTCOVIFWINFLIVTCYTLIKEIYRSTVRTRGVKGVPKCKVNVKFIIAYF 245
 Db 183 WHKASNYTFVAFWVIFLLIVFYTATKKFKSHLKSSNNSTSVKKSRRNIFIVVF 242
 Qy 246 FIGCFPFFPARITYTLESDTYDFDCTAENTLYVKESTLMTSINAQCLDPFTLCKSF 305
 Db 242 FVCFVPTHARIYFTKSGQTEAHYSCQSKEIILRYMKBFTLSSAANVCLDPIYFFLQCFF 301
 Qy 306 RNSLISMKCPNSA 319
 Db 302 REILCKKUHPLKA 315

RESULT 8
US-09-303-524A-2 ; Sequence 2, Application US / 09303524A
; Patent No. 6238B3
; GENERAL INFORMATION:
; APPLICANT: CHAMBERS, JONATHAN K.
; APPLICANT: STEWART, BRIAN R.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JIM
; APPLICANT: ARNOLD, ANNE ROMANTIC
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0
; TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
; FILE REFERENCE: GP50007
; CURRENT APPLICATION NUMBER: US/09/303,524A
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,957
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-303-524A-2

Query Match 43.4%; Score 772; DB 3; Length 338;
Best Local Similarity 47.5%; Pred. No. 1.7e-58; Mismatches 105; Indels 0; Gaps 0
Matches 149; Conservative 60; MisMatch 158; InDel 0; Gap 0

Qy 6 NLTSAPNTSLCDTYKIQVLPFLPLTVLFFGLITGLANMRFFQIRSSKSNNPPIIQLXN 65
Db 3 NSTSTQPDESCLNLITQIIPVLYCKMYEAGILNLNGSGWIFFYVSSSKSPSTIYLXN 62
Qy 66 TVISDLIMLTFPKFLSDAKIGTGPDLRTPVFCQTSVIFETMISISFISFGLTIDRYQK 125
Db 63 IIVADFWSLTFPKFLGDSGLPQWLNVFYCRVAVLFYTMNTSIVFGLSDPDRYTK 122C
Qy 126 TTRPFKTNSNPKNLLGAKILSUVIWAEMELLSLPMNMLTNRQPRDKVKKCSFLKSEFGILV 185
Db 123 IVYRPLWTFQSYVSYSQFQSYVMMILLAVPNILLTNGSVRETVQKCIELLSLGK 182
Qy 186 WHEIIVNYCQIVFWINFLIVCYTLLTKELYRSYVTRTGKVPRKVKVVKVFTIIAYF 245
Db 183 WEKASNYFVA-FWIVFLLLIVYFTTAIKFKSHLKSSRNNTSYRKCSSRNNTSIVFGLSDPDRYTK 242
Qy 246 FICFVPHFPHARFPTYLSQTRDVFDCTAENTIIFYKESTLWITSACLDPFIYFLCKSF 305
Db 243 FVCFVPHFPHARFPTYLSQTEAHYSCSQSKESKEIILRYMKFETLUSAAVCLDPFIYFLCQPP 303
Qy 306 RMSELISMILKCPNSA 319
Db 303 REFLCKKHIPKA 316

RESULT 9
US-08-988-876-3 ; Sequence 3, Application US / 089888876
; Patent No. 606596
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
 WITH IMMUNE RESPONSE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 STATE: CA
 CITY: Palo Alto
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: FF-0441 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-955-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PROSTUT09
 CLONE: 1650519
 US-08-988-876-3

Query Match 38.2%; Score 679.5; DB 3; Length 35
 Best Local Similarity 43.7%; Pred. No. 1.4e+50;
 Matches 132; Conservative 64; Mismatches 99; Indels 6

Qy	6 NTLSAPG-NTRSLCTRDKITKTVQLPPLLYTLYGLPLRTFCVQTSVIFYFTMVISIF	DB	25 NRSDGPKNTL--HNEFDITVLPVLYLIVASILNLAVLWIPFHRL
Qy	65 NTVISDLMILTEPPKILSAKLCTGPLRTFCVQTSVIFYFTMVISIF	DB	82 NIVVADLMILTEPPKIVHAGFGWYFKRILCRTSVIFYANNMVTISVF
Qy	125 KTRRPFTSNPKNLLGAKILSVVIAFMPLISIENMILNROPDKNVKKK	DB	142 KVVKPFDSRMYSTTFKVLSVCVNIMATLSPLNIIITNGQPTEDNTID
Qy	185 WHEIIVYICVTFWINFLVIVCYCLITLGELYSVYRTRGVYPRK-K	DB	202 KWHATAVYVNSCLFYAVLVILLGICYTAISRYTHS-SRGFISQSSRKXK
Qy	244 VFFTCYVPEFHFRPRTPLSQRFCTANTLTYKEESTWLTSLNACI	DB	260 VFTCFDLPYLICRMPSTFSHLRLLDESAQKILYCKEITLFLSACNVCI
Qy	304 SP 305	DB	320 SF 321

RESULT 10
US-08-467-948A-6
; Sequence 6, Application US/08467948A

Patent No. 5998164
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CBO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488-1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 293 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-948A-6

Sequence 6, Application US/08467947A
 Patent No. 6090575
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CBO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,947A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488-1140002/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 293 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-947A-6

Query Match 30.7%; Score 546.5; DB 2; Length 293;
 Best Local Similarity 42.3%; Pred. No. 2.6e-39;
 Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;

Qy 17 CTRDYKITQVFLPLIYTIVLPGVLTINGLMRIFQIRSKSNFTILFLNTVISDPLMLIT 76
 Db 15 CPDRDTTRVQLVFLPLIYTIVLPGVLTINGLMRIFQIRSKSNFTILFLNTVISDPLMLIT 76

Qy 77 FPKKILSDAKUGTGPRLTFCQVTSVIFYFTMYIISISFGLLITIDRYQKTRPFTSNSPK 136
 Db 75 LPFKKILSDHIAFWQWRAFVRCPSSVIFYEMMYGVLLGIAFRFLKTRPFLNIFIK 134

Qy 137 NLIGAKL5LSVTIWAFLPSLPNMILTNQRDKTKVKKCSFLKSEFGVTHETINYICQV 196
 Db 135 KPWGKTVSIFIWFFWFIISLPNMILSNKEATPSVTKCASLGFLGLKHMWNNICOF 194

Qy 197 IWPINFLLIVCYTLIKE---LYRSYVTRGLVGKVPRKVNKFVIIAVPFCFVP- 251
 Db 195 IFPTVFILMVEPVVTAKKMMLIESPKVRETEKTKSWKARYLISWLSSCULLHFISPE 254

Qy 252 FHPARIPYTLSQLQRDVFDCTAINTLFYVKESTLW 285
 Db 255 FHILVKPRTIRLT--VDCKI-NCLLKKQLSFW 284

Query Match 30.7%; Score 546.5; DB 3; Length 293;
 Best Local Similarity 42.3%; Pred. No. 2.6e-39;
 Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;

Qy 17 CTRDYKITQVFLPLIYTIVLPGVLTINGLMRIFQIRSKSNFTILFLNTVISDPLMLIT 76
 Db 15 CPDRDTTRVQLVFLPLIYTIVLPGVLTINGLMRIFQIRSKSNFTILFLNTVISDPLMLIT 76

Qy 77 FPKKILSDAKUGTGPRLTFCQVTSVIFYFTMYIISISFGLLITIDRYQKTRPFTSNSPK 136
 Db 75 LPFKKILSDHIAFWQWRAFVRCPSSVIFYEMMYGVLLGIAFRFLKTRPFLNIFIK 134

Qy 137 NLIGAKL5LSVTIWAFLPSLPNMILTNQRDKTKVKKCSFLKSEFGVTHETINYICQV 196
 Db 135 KPWGKTVSIFIWFFWFIISLPNMILSNKEATPSVTKCASLGFLGLKHMWNNICOF 194

Qy 197 IWPINFLLIVCYTLIKE---LYRSYVTRGLVGKVPRKVNKFVIIAVPFCFVP- 251
 Db 195 IFPTVFILMVEPVVTAKKMMLIESPKVRETEKTKSWKARYLISWLSSCULLHFISPE 254

Qy 252 FHPARIPYTLSQLQRDVFDCTAINTLFYVKESTLW 285
 Db 255 FHILVKPRTIRLT--VDCKI-NCLLKKQLSFW 284

US-08-702-344-28
 Sequence 28 Application US/08702344
 Patent No. 5723315
 APPLICANT: McCoy, John
 APPLICANT: LaVallie, Edward
 APPLICANT: Racine, Lisa
 APPLICANT: Marberg, David
 APPLICANT: Treacy, Maurice
 APPLICANT: Spaulding, Vicki
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 TITLE OF INVENTION: ENCODING THEM
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,344
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 438-8224
 TELEX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 319 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-702-344-28

Query Match 27.4%; Score 468; DB 1; Length 319;
 Best Local Similarity 34.5%; Prod. No. 2 8e-34;
 Matches 112; Conservate 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 NTSLQTRDYKIQVQLFPLLYTIVFFGLITNGIAMLRIFFQISKSNTI-IPXKNTVVISDL 71
 3 NSSFCPCPVYKQDLEP-FTYPPVYPLVIGIGSCPATWAFIQKNTNHRCSVYIYLNLTDADP 61

Db 72 LMLTFPPFKILSDAQLGTGP--LRTFVQCVTSTVTFYTMVYISISFLGTLIDRYQXTTRP 129
 62 LITALPKVIVD--LGAPWUKIIFQVIALIYNNMSTIIFLAFVSIRCLOLTHS 119

Qy 130 PTKSNPKNLGAKTSLVVIWAFMFLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEI 189
 Db 120 CKYTRIQEGFARMISTVWLMVLIIMPNMIPKDIKERENGVGCMEEFKCFGRWHLI 179

Qy 190 VNYICQVIPWNP-LIVIVCYLTKELYRSYTRTRGKVPR-KCYNKVKVIIIAVEFPI 247
 Db 180 TNFICVAF-LNFSAIILSNCLVQIYRN---KDNENYPNVKCALINILVTVGYII 234

Qy 248 CTVFHFAPIPYTISQTRDVFDCTAENTLFYKESTIMLTSNAACDPFIYFLCKSPRN 307
 235 CFVYHIVIPYPTISQTEVITDSTRISLCKTKEATULLAVSNLCDFBILYTHLSKAFRS 294

Qy 308 SLI-----SMUJKCPNSA 319
 Db 295 KVTETFASPEKTKQEKERKRCRNNAA 319

RESULT 13
 US-08-118-270-39
 Sequence 39 Application US/08118270
 GENERAL INFORMATION:
 Patient No. 5508384
 APPLICANT: Murphy, Randall B.
 APPLICANT: Schuster, David I.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BRODY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118,270
 FILING DATE: 03-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE DOCKET NUMBER: MURPHY-2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 241633-
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 326 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-118-270-39

Query Match 23.1%; Score 410.5; DB 1; Length 326;
 Best Local Similarity 32.2%; Prod. No. 1.2e-27;
 Matches 106; Conservate 65; Mismatches 137; Indels 21; Gaps 9;

Qy 27 LFPLIYTIVLFFGLITNGIAMLRIFFQISKSNTI-RSKNKF1-PLKNTVVISDLNLLFPFKILSD 84
 Db 85 AKLGTGPLETFEVQCVTSTVTFYTMVYISISFLGTLIDRYQXTTRPFTSNPKNLGAKT 144
 Db 61 SNOCNWFELRFLCNLAGIFFINTYCSAFLGTTARFAQKYPKTAQATRKRGJAL 120
 Qy 145 SVWVW---AFNPLISLPMLNLRNORDKVNKCSFLKSEFGV 194
 Db 121 SLVWVATVAASFLYMDSTNVNSKGSGNITRC-FERVEKGSKPVLITH----IC 174
 Qy 195 QVI-FWNLIVLIVCYLTKELYRSYTRTRGKVPR-KCYNKVKVIIIAVEFPIYFPI 253
 Db 175 IVGCBPTELLIFCNUVLTHTLJRGPKQQQDAEV-RRALMVCVVAVYTCVPH 233
 Qy 254 FAR-PYTYLSEOTRDVEDCPTAENTLFYKESTIMLTSNAACDPFIYFLCKSPRN 313
 Db 234 MVQLPWLAEL-GWPSSNHOAINDAQVTCUCLSTNCVLDPVYCYCTKFERKLHSEKL 292

Qy 314 KCPNSATSLSDQRKKEOGGDNEETM 312
 Db 293 NMRESSQKCSRVIDTGEMAIPIHNHFV 321

RESULT 14
 PCT-US93-08528-39
 Sequence 39, Application PCT-US93-08528
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BRONDY AND NETMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08528
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 326 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

PCT-US93-08528-39

Query Match 23.1%; Score 410.5; DB 5; Length 326;
 Best Local Similarity 32.2%; Pred. No. 1.2e-27; Mismatches 137; Indels 21; Gaps 9;
 Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

Db 1 LFPITVSIIFV,GIIANGYVWWFARLYSKKNEKIFMVNTVADLFLITPLWIVYY 60

Qy 27 DFLPLTVLFPGVGLTNGLMARIFFQI-RSKSNFI-ILENTVSDLMLPPFKLSD 84

Db 85 ARLGTOPLTRVTCQTSVIFTMISPLGLITRQKTRPFKNSNPNLGAKIL 144

Qy 61 SMQGMWFLPKFLCNLAGCLPFFINTYCSVARLGIVTYNRQAVKXPIKTAQATRKRGIAL 120

Db 145 SVVIVW---AFMFLSLSPMLNTPQDKNTYKCSPLKSEFG---LVWHEIVNYIC 194

Db 121 SIVIVVAVAAASFYVMMOSTNVNKAQSGNITRC-FERHGSKPVLIH---IC 174

Qy 195 QVI-FWNLFLIVVIVCYTLITMELYSYVVRGVCKVPRKVNVKFLIIAVFFICFVPH 253

Db 175 IVLGFFIVFLILFLCNLIVITLGPVKQRNAEV-RRRALWVCTVAVFTICFVPH 233

Qy 254 FARIPIVLSQTRDVFCTAINTLFYKESTLWTSNACLDPEFYFLCKSFNSLISM 313

Db 234 NYQLPNTLAEL-GMNPSSNHADAHQVTLCLISTNCVLDPVTCFLTKFRKHLSEKL 292

Qy 314 KCPNSATSLSDQNRKKEQDDGPNEPTM 342

Db 293 NMRSOKCSVTRDTGTEMALPINHPTV 321

RESULT 15
 US 08-988-876-9
 Sequence 9, Application US/0888876
 Patent No. 6063956
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED WITH IMMUNE RESPONSE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0441 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: GenBank
 LIBRARY: 49443
 US-08-988-876-9

Query Match 22.1%; Score 399.5; DB 3; Length 342;
 Best Local Similarity 30.7%; Pred. No. 4.3e-26; Mismatches 146; Indels 21; Gaps 9;
 Matches 103; Conservative 65; Mismatches 146; Indels 21; Gaps 9;

Qy 20 DYKITQVLEPLIYLTVLFFPGVGLTNGLMAMIFFQI--RSKSNFI-ILENTVSDLMLIT 76

Db 10 DSEFRATPLKPTVYTFVGDVYVFLGKQVYVLPKQNLVFLVPAVLFLIT 69

Qy 77 FPKKLSDAKLTGGLPRTIQCWTQSVIPLTMTSISPLPGLTIDRYQKTTREPKTSNPK 136

Db 70 LPLWIVYYSHQGNWPLPKFLCNLACCLPFTNTYCSVAFFGVITYNRQVVKPRTAQAT 129

Qy 137 NILGAKILSVIVW---APMFLSLPMLNTPQDKNTYKCSPLKSEFG---LYWH 187

Db 130 TRKGIALSLVIVWIAASFYVMDSTNVNKAQSGNITRC-FERHGSKPVLIH 188

Qy 188 BIVNIVCQV-FWNLFLIVVIVCYTLITMELYSYVVRGVCKVPRKVNVKFLIIAVFF 246

Db 189 ---1CIVLGFFIVFLILFLCNLIVITLGPVKQRNAEV-RRRALWVCTVAVFTICFVPH 242

Qy 247 IGFVPPHAFI-IPYTSQTRDVFCTAINTLFYKESTLWTSNACLDPEFYFLCKSFNSLISM 306

Db 243 ICFVPHHNQLPNTLAEI-GMWPSNHQAINDAHQVTLCILSTNCVLDPYIYCFLTKKFR 301
Qy 307 NSLIISMLKCPNSATSLSDNRKEQDGDDPNBETPM 342
Db 302 KHLSEKUNIMRSSQOKCSRVTDTGTENAIPIINHTPV 337

Search completed: February 4, 2004, 14:23:34
Job time : 22 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 14:22:16 ; Search time 37 Seconds
 (without alignments)
 1935.371 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQRDVNLNTSAAGNTSLLCTRD.....SQDNRKKEQDGGDPNEETPM 342

Scoring table: BLOSUM62

Gapext 0.5

Searched: 801455 seeds, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA: *

```

 1: /cgns2_6/picodata/1/pubpaas/US07_PUBCOMB.pep:*
 2: /cgns2_6/picodata/1/pubpaas/2CT_PUB.PEP:*
 3: /cgns2_6/picodata/1/pubpaas/US06_NEW_PUB.PEP:*
 4: /cgns2_6/picodata/1/pubpaas/US05_PUBCOMB.PEP:*
 5: /cgns2_6/picodata/1/pubpaas/US05_PUBCOMB.PEP:*
 6: /cgns2_6/picodata/1/pubpaas/PECTUS_PUBCOMB.Pep:*
 7: /cgns2_6/picodata/1/pubpaas/US08_NEW_PUB.PEP:*
 8: /cgns2_6/picodata/1/pubpaas/US08_PUBCOMB.PEP:*
 9: /cgns2_6/picodata/1/pubpaas/US09_PUBCOMB.PEP:*
10: /cgns2_6/picodata/1/pubpaas/US09C_PUBCOMB.PEP:*
11: /cgns2_6/picodata/1/pubpaas/US09C_PUBCOMB.PEP:*
12: /cgns2_6/picodata/1/pubpaas/US09_NEW_PUB.PEP:*
13: /cgns2_6/picodata/1/pubpaas/US10A_PUBCOMB.PEP:*
14: /cgns2_6/picodata/1/pubpaas/US10B_PUBCOMB.PEP:*
15: /cgns2_6/picodata/1/pubpaas/US10C_PUBCOMB.PEP:*
16: /cgns2_6/picodata/1/pubpaas/US10C_NEW_PUB.PEP:*
17: /cgns2_6/picodata/1/pubpaas/US60_NEW_PUB.PEP:*
18: /cgns2_6/picodata/1/pubpaas/US60_PUBCOMB.PEP:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1778	US-09-835-922-2	342	9	US-09-835-922-2	Sequence 2, Appli
2	1778	US-09-827-93A-2	342	9	US-09-827-93A-2	Sequence 2, Appli
3	1778	US-09-780-576-2	342	9	US-09-780-576-2	Sequence 2, Appli
4	1778	US-09-964-008-1	342	10	US-09-964-008-1	Sequence 1, Appli
5	1778	X	342	12	US-10-272-983-32	Sequence 32, Appli
6	1778	X	342	12	US-09-745-842-6	Sequence 6, Appli
7	1778	X	342	12	US-10-333-807-32	Sequence 32, Appli
8	1778	X	342	12	US-10-417-822-34	Sequence 34, Appli
9	1778	X	342	15	US-10-225-56A-63	Sequence 643, Appli
10	1748	X	342	15	US-10-333-844-2	Sequence 2, Appli
11	1748	X	342	10	US-09-964-008-3	Sequence 3, Appli
12	1634	X	315	12	US-09-745-42-4	Sequence 4, Appli
13	1528.5	X	343	12	US-09-745-842-2	Sequence 2, Appli
14	1237.5	X	267	12	US-09-745-842-2	Sequence 12, Appli
15	829	X	333	11	US-09-924-125-2	Sequence 2, Appli

RESULTS

1 US-09-835-922-2

Sequence 2, Application US/09835922

Patent No. US20010046497A1

GENERAL INFORMATION:

APPLICANT: Luo, Lin

APPLICANT: Gustafson, Eric

APPLICANT: Liu, Yan-Hui

APPLICANT: Chen, Guodong

TITLE OF INVENTION: G-Protein Coupled Receptor and Methods

FILE REFERENCE: CN01167K

CURRENT FILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: US 60/199, 041

NUMBER OF SEQ ID NO: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 2

LENGTH: 342

TYPE: PRT

ORGANISM: homo sapiens

US-09-835-922-2

Query Match 100.0% ; Score 1778; DB 9; Length 342;

Best Local Similarity 100.0% ; Pred. No. 8.1e-159;

Matches 342; Conservative 0; Indels 0; Gaps 0;

Qy 1 MQAVDNLTAAAGNTSLCPRDYKITQVLFPPLTVLFFVGLITNGLMRIFQIRSKSNFI 60

Ds 1 MQAVDNLTAAAGNTSLCPRDYKITQVLFPPLTVLFFVGLITNGLMRIFQIRSKSNFI 60

Qy 61 IFLAKNTVISDMLMTFPKILSDAKLGTPRLTIVYTMISISPLGLITI 120

Ds 61 IFLAKNTVISDMLMTFPKILSDAKLGTPRLTIVYTMISISPLGLITI 120

Qy 121 DRYQTTRPKTSNPKNNLQGAKLSSVVAWFMLLSPLNMILTRQPRDKNYKKCSPLKs 180

ALIGNMENTS

1

Db 121 DRYQKTRPFKTSNPKNLGAKILSVVVIWAFMFLSLPNNMLTNRQPRDKVTKRGSFLKS 180
 Qy 181 EFGLVWHEIVNYICQVIFWINFLLIVIVCYTLTKEVLRSYVTRGVGKVPKKAVKVFI 240
 Db 181 EFGLVWHEIVNYICQVIFWINFLLIVIVCYTLTKEVLRSYVTRGVGKVPKKAVKVFI 240
 Qy 241 IIAVFFICVFPHFARIPIYTLISQTRDVFCTAENTLYFVKESTLWLTSLNACLDPIYFF 300
 Db 241 IIAVFFICVFPHFARIPIYTLISQTRDVFCTAENTLYFVKESTLWLTSLNACLDPIYFF 300
 Qy 301 LCKSFRNSLISMUKCPNSATSLSDNRKKEQDGDPNEETPM 342
 Db 301 LCKSFRNSLISMUKCPNSATSLSDNRKKEQDGDPNEETPM 342

RESULT 2
 Sequence 2, Application US/09827937A
 Patent No. US20020052043A1
 GENERAL INFORMATION:
 APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: Human G-Protein Coupled Receptors
 FILE REFERENCE: 1488.1220003
 CURRENT APPLICATION NUMBER: US/09/827,937A
 CURRENT FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 08/852,824
 PRIOR FILING DATE: 1997-05-07
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-827-937A-2

Query Match Score 1778; DB 9; Length 342;
 Best Local Similarity 100.0%; Pred. No. 8.1e-159; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
 Qy 1 MQAVDNLTSGAGNTSLCTRDYKITQVLFPFLYYTLLFFGLTINGLAMRIFQIRSKSNFI 60
 Db 1 MQAVDNLTSGAGNTSLCTRDYKITQVLFPFLYYTLLFFGLTINGLAMRIFQIRSKSNFI 60
 Qy 61 IFLKNTVISDLMLTFPFKILSDAKLGTGPLRTFVQCVTSVLFYTMVTSISFLGLITI 120
 Db 61 IFLKNTVISDLMLTFPFKILSDAKLGTGPLRTFVQCVTSVLFYTMVTSISFLGLITI 120
 Qy 121 DRYQKTRPFKTSNPKNLGAKILSVVVIWAFMFLSLPNNMLTNRQPRDKVTKRGSFLKS 180
 Db 121 DRYQKTRPFKTSNPKNLGAKILSVVVIWAFMFLSLPNNMLTNRQPRDKVTKRGSFLKS 180
 Qy 181 EFGLVWHEIVNYICQVIFWINFLLIVIVCYTLTKEVLRSYVTRGVGKVPKKAVKVFI 240
 Db 181 EFGLVWHEIVNYICQVIFWINFLLIVIVCYTLTKEVLRSYVTRGVGKVPKKAVKVFI 240
 Qy 241 IIAVFFICVFPHFARIPIYTLISQTRDVFCTAENTLYFVKESTLWLTSLNACLDPIYFF 300
 Db 241 IIAVFFICVFPHFARIPIYTLISQTRDVFCTAENTLYFVKESTLWLTSLNACLDPIYFF 300
 Qy 301 LCKSFRNSLISMUKCPNSATSLSDNRKKEQDGDPNEETPM 342
 Db 301 LCKSFRNSLISMUKCPNSATSLSDNRKKEQDGDPNEETPM 342

RESULT 3
 US-09-780-576-2
 Sequence 2, Application US/0980576
 Patent No. US20020072072A1
 GENERAL INFORMATION:
 Civeilli, Olivier
 APPLICANT: No. US20020072072A1hacker, Hans-Peter
 APPLICANT: Wang, Zhiwei

Query Match Score 1778; DB 9; Length 342;
 Best Local Similarity 100.0%; Pred. No. 8.1e-159; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
 Qy 1 MQAVDNLTSGAGNTSLCTRDYKITQVLFPFLYYTLLFFGLTINGLAMRIFQIRSKSNFI 60
 Db 1 MQAVDNLTSGAGNTSLCTRDYKITQVLFPFLYYTLLFFGLTINGLAMRIFQIRSKSNFI 60
 Qy 61 IFLKNTVISDLMLTFPFKILSDAKLGTGPLRTFVQCVTSVLFYTMVTSISFLGLITI 120
 Db 61 IFLKNTVISDLMLTFPFKILSDAKLGTGPLRTFVQCVTSVLFYTMVTSISFLGLITI 120
 Qy 121 DRYQKTRPFKTSNPKNLGAKILSVVVIWAFMFLSLPNNMLTNRQPRDKVTKRGSFLKS 180
 Db 121 DRYQKTRPFKTSNPKNLGAKILSVVVIWAFMFLSLPNNMLTNRQPRDKVTKRGSFLKS 180
 Qy 181 EFGLVWHEIVNYICQVIFWINFLLIVIVCYTLTKEVLRSYVTRGVGKVPKKAVKVFI 240
 Db 181 EFGLVWHEIVNYICQVIFWINFLLIVIVCYTLTKEVLRSYVTRGVGKVPKKAVKVFI 240
 Qy 241 IIAVFFICVFPHFARIPIYTLISQTRDVFCTAENTLYFVKESTLWLTSLNACLDPIYFF 300
 Db 241 IIAVFFICVFPHFARIPIYTLISQTRDVFCTAENTLYFVKESTLWLTSLNACLDPIYFF 300
 Qy 301 LCKSFRNSLISMUKCPNSATSLSDNRKKEQDGDPNEETPM 342
 Db 301 LCKSFRNSLISMUKCPNSATSLSDNRKKEQDGDPNEETPM 342

Query Match Score 1778; DB 10; Length 342;
 Best Local Similarity 100.0%; Pred. No. 8.1e-159; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
 Qy 1 MQAVDNLTSGAGNTSLCTRDYKITQVLFPFLYYTLLFFGLTINGLAMRIFQIRSKSNFI 60
 Db 1 MQAVDNLTSGAGNTSLCTRDYKITQVLFPFLYYTLLFFGLTINGLAMRIFQIRSKSNFI 60

Qy 61 IFLKNTVISDLAMILTPFPKILSDAKLGTGPLRTFVQCVTSVIFTMYISIISPLGLITI 120
 61 IFLKNTVISDLAMILTPFPKILSDAKLGTGPLRTFVQCVTSVIFTMYISIISPLGLITI 120
 Db 121 DRYQKTRPFKTSNPNLGAKILSVVIAFMFLSLPNMILTRQPRDKNVKCSFLKS 180
 Qy 121 DRYQKTRPFKTSNPNLGAKILSVVIAFMFLSLPNMILTRQPRDKNVKCSFLKS 180
 Db 121 DRYQKTRPFKTSNPNLGAKILSVVIAFMFLSLPNMILTRQPRDKNVKCSFLKS 180
 Qy 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Db 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Qy 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Db 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Qy 241 IIAVEFFCVPFHARIPYTSQTRDFTCAENTLYVKESTLWLTSLNACLDPPFYF 300
 Db 241 IIAVEFFCVPFHARIPYTSQTRDFTCAENTLYVKESTLWLTSLNACLDPPFYF 300
 Qy 241 IIAVEFFCVPFHARIPYTSQTRDFTCAENTLYVKESTLWLTSLNACLDPPFYF 300
 Db 301 LCKSFRNSLISMKCPNSATSLSQDNRKKEODGGDNEETPM 342
 Qy 301 LCKSFRNSLISMKCPNSATSLSQDNRKKEODGGDNEETPM 342
 Db 301 LCKSFRNSLISMKCPNSATSLSQDNRKKEODGGDNEETPM 342

RESULT 5
 US-10-272-983-32
 Sequence 32, Application US/10272983
 Publication No. US20103048450A1
 GENERAL INFORMATION:
 APPLICANT: Chen, Ruoping
 APPLICANT: Dang, Huong T.
 APPLICANT: Liaw, Chen W.
 APPLICANT: Lin, I-Lin
 TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 FILE REFERENCE: AREN0050
 CURRENT APPLICATION NUMBER: US/10/272,983
 CURRENT FILING DATE: 2002-10-17
 PRIOR APPLICATION NUMBER: US/09/417,044
 PRIOR FILING DATE: 1999-10-12
 PRIOR APPLICATION NUMBER: 60/109,213
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
 PRIOR APPLICATION NUMBER: 60/121,851
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/123,946
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,949
 PRIOR APPLICATION NUMBER: 60/136,436
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/136,437
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/136,439
 PRIOR FILING DATE: 1999-05-28
 PRIOR FILING DATE: 1999-05-28
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOs: 74
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 32
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-272-983-32

RESULT 6
 US 09-745-842-6
 Sequence 6, Application US/09745842
 Publication No. US2010304777A1
 GENERAL INFORMATION:
 APPLICANT: Conley, Pamela B.
 APPLICANT: Jantzen, Hans-Michael
 APPLICANT: Ramakrishnan-Dubridge, Vanitha
 APPLICANT: Julius, David
 APPLICANT: Hollerer, Gunter
 APPLICANT: COR Therapeutics, Inc.
 TITLE OF INVENTION: P2712 Receptor
 FILE REFERENCE: 44481-5053-US
 CURRENT APPLICATION NUMBER: US/09/745,842
 CURRENT FILING DATE: 2000-12-26
 PRIOR FILING DATE: 1999-12-23
 NUMBER OF SEQ ID NOs: 21
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Homo sapiens
 US 09-745-842-6

Query Match 100.0%; Score 1778; DB 12; Length 342;
 Best Local Similarity 100.0%; Pred. No. 8..1e-159; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0; Del 0; Gap 0;

Qy 1 MQAVDNLTSAPGNTSLCDRDXKITQVLFPLIYTVLFFVGLITNGLMARIPOIRSKSNFI 60
 Db 1 MQAVDNLTSAPGNTSLCDRDXKITQVLFPLIYTVLFFVGLITNGLMARIPOIRSKSNFI 60
 Qy 61 IFLKNTVISDLAMILTPFPKILSDAKLGTGPLRTFVQCVTSVIFTMYISIISPLGLITI 120
 Db 61 IFLKNTVISDLAMILTPFPKILSDAKLGTGPLRTFVQCVTSVIFTMYISIISPLGLITI 120
 Qy 121 DRYQKTRPFKTSNPNLGAKILSVVIAFMFLSLPNMILTRQPRDKNVKCSFLKS 180
 Db 121 DRYQKTRPFKTSNPNLGAKILSVVIAFMFLSLPNMILTRQPRDKNVKCSFLKS 180
 Qy 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Db 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Qy 241 IIAVEFFCVPFHARIPYTSQTRDFTCAENTLYVKESTLWLTSLNACLDPPFYF 300
 Db 241 IIAVEFFCVPFHARIPYTSQTRDFTCAENTLYVKESTLWLTSLNACLDPPFYF 300
 Qy 301 LCKSFRNSLISMKCPNSATSLSQDNRKKEODGGDNEETPM 342
 Db 301 LCKSFRNSLISMKCPNSATSLSQDNRKKEODGGDNEETPM 342

Query Match 100.0%; Score 1778; DB 12; Length 342;
 Best Local Similarity 100.0%; Pred. No. 8..1e-159; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0; Del 0; Gap 0;

Qy 1 MQAVDNLTSAPGNTSLCDRDXKITQVLFPLIYTVLFFVGLITNGLMARIPOIRSKSNFI 60
 Db 1 MQAVDNLTSAPGNTSLCDRDXKITQVLFPLIYTVLFFVGLITNGLMARIPOIRSKSNFI 60
 Qy 61 IFLKNTVISDLAMILTPFPKILSDAKLGTGPLRTFVQCVTSVIFTMYISIISPLGLITI 120
 Db 61 IFLKNTVISDLAMILTPFPKILSDAKLGTGPLRTFVQCVTSVIFTMYISIISPLGLITI 120
 Qy 121 DRYQKTRPFKTSNPNLGAKILSVVIAFMFLSLPNMILTRQPRDKNVKCSFLKS 180
 Db 121 DRYQKTRPFKTSNPNLGAKILSVVIAFMFLSLPNMILTRQPRDKNVKCSFLKS 180
 Qy 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Db 181 EFGLVWHEIVNVIQCVTFWINFLLIVCYTLTKELYRSYTRTRGVGVKVRKVNKVFI 240
 Qy 241 IIAVEFFCVPFHARIPYTSQTRDFTCAENTLYVKESTLWLTSLNACLDPPFYF 300
 Db 241 IIAVEFFCVPFHARIPYTSQTRDFTCAENTLYVKESTLWLTSLNACLDPPFYF 300
 Qy 301 LCKSFRNSLISMKCPNSATSLSQDNRKKEODGGDNEETPM 342
 Db 301 LCKSFRNSLISMKCPNSATSLSQDNRKKEODGGDNEETPM 342

Page 4

Sequence 643, Application US/10225567A
 GENERAL INFORMATION: Publication No. US20030113798A1
 APPLICANT: Lifespan Biosciences
 BROWN, Joseph P.
 APPLICANT: Burner, Glenn C.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIgenic PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225, 567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257, 144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2252
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 643
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-225, 567A-643

Query Match Score 100.0%; Best Local Similarity 100.0%; Prod. No. 8.1e-159; Length 342;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQDNLTSGPNTSLC TDYK TQVLFPLLYTVLFFGLTNGLMRIFQFIRSKNF 60
 Db 1 MAQDNLTSGPNTSLC TDYK TQVLFPLLYTVLFFGLTNGLMRIFQFIRSKNF 60

Qy 61 IFLKNTVISPLMLTFPKILSDAKLGTGPIRTFCVQTSIFYFTMYSISFLGLITI 120
 Db 61 IFLKNTVISPLMLTFPKILSDAKLGTGPIRTFCVQTSIFYFTMYSISFLGLITI 120

Qy 61 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180
 Db 61 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180

Qy 121 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 121 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180
 Db 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180

Qy 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180
 Db 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180

Qy 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180
 Db 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180

Qy 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 301 LCKSPRNLSLIMKCPNSATSLSDNRAKEQDGDPNEETPM 342
 Db 301 LCKSPRNLSLIMKCPNSATSLSDNRAKEQDGDPNEETPM 342

RESULT 10 -
 US-10-333-844-2.rapb
 Sequence 2, Application US/10333844
 GENERAL INFORMATION:
 Publication No. US20030124626A1
 APPLICANT: Yamamotochi Pharmaceutical Co., Ltd.
 TITLE OF INVENTION: Method for screening antiplatelet agents
 FILE REFERENCE: Y0122PCM-656
 CURRENT APPLICATION NUMBER: US10/333, 844
 CURRENT FILING DATE: 2003-01-24
 PRIOR APPLICATION NUMBER: JP 2000-334721
 PRIOR FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: JP 2001-3577
 PRIOR FILING DATE: 2001-01-11
 NUMBER OF SEQ ID NOS: 12
 SEQ ID NO: 2
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-333-844-2

Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 8.1e-159; Length 342;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQDNLTSGPNTSLC TDYK TQVLFPLLYTVLFFGLTNGLMRIFQFIRSKNF 60
 Db 1 MAQDNLTSGPNTSLC TDYK TQVLFPLLYTVLFFGLTNGLMRIFQFIRSKNF 60

Qy 61 IFLKNTVISPLMLTFPKILSDAKLGTGPIRTFCVQTSIFYFTMYSISFLGLITI 120
 Db 61 IFLKNTVISPLMLTFPKILSDAKLGTGPIRTFCVQTSIFYFTMYSISFLGLITI 120

Qy 61 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180
 Db 61 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180

Qy 121 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 121 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180
 Db 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180

Qy 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180
 Db 121 DRYQTTTRFKTSKPNLIGAKLSSVWAFMPLSLPNMILTRQPDKVNKKCSPLKS 180

Qy 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240
 Db 181 EFLGYWHEIVNYICQVTFINFLIVIVCYTLTKEVLRSYVTRGCKVPRKVKVFI 240

Qy 301 LCKSPRNLSLIMKCPNSATSLSDNRAKEQDGDPNEETPM 342
 Db 301 LCKSPRNLSLIMKCPNSATSLSDNRAKEQDGDPNEETPM 342

RESULT 12
 US-09-745-842-4
 ; Sequence 4, Application US/09745842
 ; Publication No. US20030170777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conley, Pamela A.
 ; APPLICANT: Jantzen, Hans-Michael
 ; APPLICANT: Ramakrishnan-DuBridge, Vanitha
 ; APPLICANT: Hollopeter, Gunter
 ; APPLICANT: COR Therapeutics, Inc.
 ; TITLE OF INVENTION: P2Y12 Receptor
 ; FILE REFERENCE: 44481-5053-US
 ; CURRENT APPLICATION NUMBER: US/09745842
 ; CURRENT FILING DATE: 2000-12-26
 ; PRIOR APPLICATION NUMBER: US 60/171,622
 ; PRIOR FILING DATE: 1999-12-23
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 315
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-745-842-4

Query Match 91 9%; Score 1634; DB 12; Length 315;
 Best Local Similarity 100.0%; Pred. No. 2.5e-145;
 Matches 315; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 MAQDNLTSPGNTSLCTRDYKITQVLPFLTYTLPFGTLINGLANRIFQIRSKNSNFI 60
 Db 1 MAQDNLTSPGNSLCTRDYKITQVLPFLTYTLPFGTLINGLANRIFQIRSKNSNFI 60

Query Match 91 9%; Score 1634; DB 12; Length 315;
 Best Local Similarity 100.0%; Pred. No. 2.5e-145;
 Matches 315; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 61 FLKNTVISDMLLTFFPKILSDAKLGTPFLTRFVQVTSVIFYFTMYISFPLGHTI 120
 Db 61 FLKNTVISDMLLTFFPKILSPAKLGTPFLTRFVQVTSVIFYFTMYISFPLGHTI 120

Qy 121 DRYQTRPFTNSPKNLGAKILSUVVIAWMPFLSPNMILTRQPDKNYKCSPLKS 180
 Db 121 DRYQTRPFTNSPKNLGAKILSUVVIAWMPFLSPNMILTRQPDKNYKCSPLKS 180

Qy 181 EFGLYWHEINYCQVTFINFLLIVCYTLTKELYSYVRTRGVGVYPRCKVVF1 240
 Db 181 EFGLYWHEINYCQVTFINFLLIVCYTLTKELYSYVRTRGVGVYPRCKVVF1 240

Qy 241 IIAVFFICYPFHARIPTYLSSCTRDVFCTAENTLFYVKESTLWLTSLNACDPFLYFF 300
 Db 241 IIAVFFICYPFHARIPTYLSSCTRDVFCTAENTLFYVKESTLWLTSLNACDPFLYFF 300

Qy 301 LCKSPNSLISMLKC 315
 Db 301 LCKSPNSLISMLKC 315

RESULT 13
 US-09-745-842-2
 ; Sequence 2, Application US/09745842
 ; Publication No. US20030170777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conley, Pamela A.
 ; APPLICANT: Jantzen, Hans-Michael
 ; APPLICANT: Ramakrishnan-DuBridge, Vanitha
 ; APPLICANT: Hollopeter, Gunter
 ; APPLICANT: COR Therapeutics, Inc.
 ; TITLE OF INVENTION: P2Y12 Receptor
 ; FILE REFERENCE: 44481-5053-US
 ; CURRENT APPLICATION NUMBER: US/09745842
 ; CURRENT FILING DATE: 2000-12-26

```

Db   61 IFLNTVSDLMNLTPPKILSPAKLGTGPRTFVCOVTSIYFMYISSSPLGLITI 120
QY  121 DRYOKTTRPKTSNPKNLIGAKLISWVIAWFMLISPNMILNRPDKATVKKCSFLKS 180
Db   121 DRYOKTTRPKTSNPKNLIGAKLISWVIAWFMLISPNMILNRPDKATVKKCSFLKS 180
QY  181 EFGLYWHELVNYICQVIVNLLIVCYLTKEIYRSYVTRGVKPVKRNKVKF 240
Db   181 EFGLYWHELVNYICQVIVNLLIVCYLTKEIYRSYVTRGVKPVKRNKVKF 240
QY  241 IIAVFFI-GFPFF 252
Db   241 HCCCLYLFCSPFF 253

```

```

RESULT 15
US-09-924-125-2
Sequence 2, Application US/09924125
; Publication No. US20030050235A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: THE NATURAL LIGAND FOR ORPHAN G PROTEIN COUPLED RECEPTOR GPR86 AN
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 909-092
; CURRENT APPLICATION NUMBER: US/09/924-125
; CURRENT FILING DATE: 2001-07-08
; PRIOR APPLICATION NUMBER: US 09/924,125
; PRIOR FILING DATE: 2001-07-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-924-125-2

Query Match      46.6% Score 829; DB 11; Length 333;
Best Local Similarity 49.1%; Pred. No. 1.1e-69;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;
QY  17 CTDROYKIQVLFPLVYLFPGVLITGLAMIFFQIRSKSNSPFIILKLNTVSDLMILT 76
Db   15 CPTDTRIVQLVFLPALYTIVFLTGILNLALMVVHPPSSSTVIIYKLNTVADLIMTL 74
QY  77 FPFKILSDAKLGTOPRTEVCOVTSIVFYFMYTISISFLGLITIDRYKQTTRPKTSNPK 136
Db   75 LPFKILSLSHLAPWQLRFPVCRSSVIVYETIVNGIVVIGLIAFDPLKTRPLNIFLK 134
QY  137 NLIGAKLISWVIAWFMLISPNMILNRPDKATVKKCSFLKSFGLVHENVYICQV 196
Db   135 KPVPAKTVSIFTWFLF2SLPANILSKEATPSVVKCASTGPGLKHQMANNICQF 194
QY  197 IFWTNFLIVVCTPLTKELYRSYVPTCGVKGPRKVNQVFLIAVPTICEVDFHAR 256
Db   195 FFWTFILMFLVFTVIAKRYDYSRKSKDKRNKCLEGKCFVVAVFFOFAPPHFAR 254
QY  257 IPYTLSQRFDVECTAENTLPTKESTIWLTSINAUDPPIYPLICKSFNSLISMKCP 316
Db   255 VPYTHSOTANKTDERLQOLFIRETTFLFLATTNICMDPLTIFLCKKFTKLPCMQ--G 312
QY  317 NSATSLSQDNRKEDQ 332
Db   313 RFTPASQENHSSATD 328

```

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 14:23:06 ; search time 43 Seconds

(without alignments)
 1232.430 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778
 Sequence: 1 MQAYDNLITSAPGNTSLLCTRD.....SQDNRKKEQDGDPNERTPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
 Listing First 45 summaries

1107863

Database : A_Geneseq_19Jun03:
 1: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq-emb/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq-emb/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseq-emb/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseq-emb/AA2003.DAT:*

RESULT 1

ID AAW81576

Standard; Protein; 342 AA.

XX

AAW1576;

AC

XX

DT

22-FEB-1999 (first entry)

DE EBV-induced G-protein coupled receptor (EBI-2) polypeptide.

XX

KW induced G-protein coupled receptor; EBI-2; Epstein-Barr Virus; ulcer;

XX

KW endotheium-differentiation gene; EDG-1-like G-protein coupled receptor;

XX

KW recombinant; agonist; asthma; Parkinson's disease; heart failure; asthma;

XX

KW hypertension; urinary retention; osteoporosis; antagonist; hypertension;

XX

KW angina pectoris; myocardial infarction; allergy; psychosis; depression;

XX

KW migraine; vomiting; stroke; eating disorder;migraine headache; cancer;

XX

OS Homo sapiens.

XX

Key Misc-difference 6

FT FT /note= "encoded by ARC"

XX

Misc-difference 14

FT FT /note= "encoded by ARC"

XX

PN WO9850549-A2.

XX

PD 12-NOV-1998.

XX

PF 07-MAY-1998;

XX

98WO-US09048

Pred. No. is the number of results predicted by chance to have a a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result % Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
-1	1778	100.0	342	20	AAW81576		BBV-induced G-protein coupled receptor (EBI-2) polypeptide.
2	1778	100.0	342	21	ABP0236	AAM48353	Human G protein-co receptor; Human PAFR3; prokaryotic; Human P2Y12; Plant Macaque ortholog; Murine G protein-C receptor; Rat P2-purinergic receptor; Rat M8-10 receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human CON203 G protein; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Human UDP-GlcNAc kinase; Chemokine receptor; Human HNEA81 poly amino acid sequence; Human UDP-GlcNAc kinase; Human stem cell G-protein; Human KIAA0001 receptor; Human UDP-GlcNAc kinase; Human stem cell G-protein; Human endonutri-
3	1778	100.0	342	21	AAE04385	AAM48354	Human G protein-C receptor; Human P2-purinergic receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human HNEA81 poly amino acid sequence; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Chemokine receptor; Human UDP-GlcNAc kinase; Chemokine receptor; Mouse G protein-coupled receptor; Mouse stem cell G-protein; Human EBV-induced protein SEQ; Human protein sequence
4	1778	100.0	342	22	AAE04384	AAM48355	Human G protein-C receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human HNEA81 poly amino acid sequence; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Chemokine receptor; Mouse G protein-coupled receptor; Mouse stem cell G-protein; Human EBV-induced protein SEQ; Human protein sequence
5	1778	100.0	342	22	AAE04383	AAM48356	Human G protein-C receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human HNEA81 poly amino acid sequence; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Chemokine receptor; Mouse G protein-coupled receptor; Mouse stem cell G-protein; Human EBV-induced protein SEQ; Human protein sequence
6	1778	100.0	342	22	AAE04382	AAM48357	Human G protein-C receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human HNEA81 poly amino acid sequence; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Chemokine receptor; Mouse G protein-coupled receptor; Mouse stem cell G-protein; Human EBV-induced protein SEQ; Human protein sequence
7	1778	100.0	342	23	AAE04381	AAM48358	Human G protein-C receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human HNEA81 poly amino acid sequence; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Chemokine receptor; Mouse G protein-coupled receptor; Mouse stem cell G-protein; Human EBV-induced protein SEQ; Human protein sequence
8	1778	100.0	342	23	AAE04380	AAM48359	Human G protein-C receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human HNEA81 poly amino acid sequence; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Chemokine receptor; Mouse G protein-coupled receptor; Mouse stem cell G-protein; Human EBV-induced protein SEQ; Human protein sequence
9	1778	100.0	342	23	AAU80164		Human G protein-C receptor; Human P2-purinergic receptor; Human hemokine receptor; Human G protein co receptor; Novel human G protein-coupled receptor; Human HNEA81 poly amino acid sequence; Human GPCR polypeptide; Human 7-transmembrane receptor; Human chemokine receptor; Chemokine receptor; Mouse G protein-coupled receptor; Mouse stem cell G-protein; Human EBV-induced protein SEQ; Human protein sequence

PR 07-MAY-1997; 97US-0852824.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA PI Li Y, Rubin SM;
 XX DR WPI; 1999-034722/03.
 DR N-PSDB; AAV69760.
 XX PT New isolated human G-protein coupled receptors - used to develop
 PT products for treating e.g. asthma, Parkinson's disease, heart
 PT failure, osteoporosis, hypertension, psychoses, eating disorders or
 PT cancers
 PS Claim 1; Fig 1A-C; 65pp; English.
 XX This represents a EBV-induced G-protein coupled receptor (EBI-2)
 CC polypeptide. The encoding DNA is deposited under the accession number
 CC ATCC No: 209003. The invention provides two human G-protein coupled
 CC receptor polypeptides. The polypeptides are human Epstein-Barr Virus
 CC (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide
 CC and a human endothelin-differentiation gene (EDG) like G-protein coupled
 CC receptor, designated EDG-1 like G-protein coupled receptor. Vectors
 CC comprising the EBI-2 and EDG-1-like polypeptides encoding DNA can be used
 CC to recombinant production of the proteins
 CC Agonists for G-protein coupled receptors can be used for the treatment of
 CC asthma, Parkinson's disease, acute heart failure, hypertension, urinary
 CC retention and osteoporosis. Antagonists can be used for the treatment of
 CC hypertension, angina Pectoris, myocardial infarction, ulcers, asthma,
 CC allergies, psychoses, depression, migraine, vomiting, stroke, eating
 CC disorders, migraine headaches, cancer and benign Prostatic hypertrophy
 CC screening
 XX Sequence 342 AA;
 SQ Query Match 100.0%; Score 1778; DB 20; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT
 Qy 1 MQAVDNLTSAGNTSLCSTDYKITYQLFPLLYTVLFFVGLITNLAMLIFFQTRSKNSKFI 60
 Db 1 MQAVDNLTSAGNTSLCSTDYKITYQLFPLLYTVLFFVGLITNLAMLIFFQTRSKNSKFI 60
 Qy 61 IFLKNTVISDLIMLTTFPKLSDAKLGTPSPRLTVCQTVSIVTYFTMVISISPLGLITI 120
 Db 61 IFLKNTVISDLIMLTTFPKLSDAKLGTPSPRLTVCQTVSIVTYFTMVISISPLGLITI 120
 Ps Qy 121 DRYQKTRPFTSNPKNLGKILSYVIAWMFLISLPDNMLTRQPDKNVRKCSPLKS 180
 Db 121 DRYQKTRPFTSNPKNLGKILSYVIAWMFLISLPDNMLTRQPDKNVRKCSPLKS 180
 Qy 181 FEGLYWHEIIVYICQIVFWINFLIVCYCTLITKELYRSYVRTGVGVKPRKUNVKVFI 240
 Db 181 FEGLYWHEIIVYICQIVFWINFLIVCYCTLITKELYRSYVRTGVGVKPRKUNVKVFI 240
 Qy 241 IIAVFFCFVPEHARIPYTSQTRDVEDCTAENTLFYKESTWLTSNALCDPFIYFF 300
 Db 241 IIAVFFCFVPEHARIPYTSQTRDVEDCTAENTLFYKESTWLTSNALCDPFIYFF 300
 Qy 301 LCKSFANSLSIMLKCPNSATLSQDNRKKEQDGDPNEETPM 342
 Db 301 LCKSFANSLSIMLKCPNSATLSQDNRKKEQDGDPNEETPM 342

RESULT 2
 AAY71306 standard; Protein; 342 AA.
 ID AAY71306
 XX AC AAY71306;
 XX DT 02-NOV-2000 (first entry)

Query Match 100.0%; Score 1778; DB 21; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQAVDNLTSAGNTSLCSTDYKITYQLFPLLYTVLFFVGLITNLAMLIFFQTRSKNSKFI 60

QY

DE Human orphan G protein-coupled receptor hCHN8.
 XX Human; orphan G protein-coupled receptor; GPCR; hCHN8; drug screening;
 KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
 XX OS Homo sapiens.
 XX PN WO200031258-A2.
 XX PD 02-JUN-2000.
 XX PF 13-OCT-1999; 99WO-US23687.
 XX PR 20-NOV-1998; 99US-0109213.
 XX PR 16-FEB-1999; 99US-0120416.
 XX PR 26-FEB-1999; 99US-011852.
 XX PR 12-MAR-1999; 99US-0123946.
 XX PR 12-MAR-1999; 99US-0123949.
 XX PR 28-MAY-1999; 99US-0136436.
 XX PR 28-MAY-1999; 99US-0136437.
 XX PR 28-MAY-1999; 99US-0136439.
 XX PR 28-MAY-1999; 99US-0136567.
 XX PR 28-MAY-1999; 99US-0137127.
 XX PR 28-MAY-1999; 99US-0137131.
 XX PR 29-JUN-1999; 99US-0141448.
 XX PR 29-SEP-1999; 99US-0156555.
 XX PR 29-SEP-1999; 99US-0156633.
 XX PR 29-SEP-1999; 99US-0156634.
 XX PR 29-SEP-1999; 99US-0156635.
 XX PR 01-OCT-1999; 99US-0157280.
 XX PR 01-OCT-1999; 99US-0157281.
 XX PR 01-OCT-1999; 99US-0157282.
 XX PR 01-OCT-1999; 99US-0157293.
 XX PR 01-OCT-1999; 99US-0157294.
 XX PR 12-OCT-1999; 99US-0416700.
 XX PR 12-OCT-1999; 99US-0417044.
 XX PA (AREN-) ARENA PHARM INC.
 XX PT Chen R, Dang HT, Liaw CW, Lin I;
 XX DR WPI; 2000-400058/34.
 XX DR N-PSDB; AAD01133.

XX Novel human orphan G protein-coupled receptors and the encoding cDNAs
 PT for use in the identification of G protein-coupled receptor agonists -
 XX Claim 62; Page 82-83; 102pp; English.

The present amino acid sequence is the hCHN8, an endogenous human
 CC orphan G protein coupled receptor (GPCR) expressed in left and right
 CC cerebellum, kidney and lung. The hCHN8 cDNA was identified using full
 CC length EST (expressed sequence tag) 764455 as a probe.
 CC The orphan GPCR of the invention, like all GPCRs
 CC alpha helices with an extracellular N-terminus and an intracellular
 CC C-terminus. However, no endogenous ligands has yet been identified for
 CC the proteins of the invention. The orphan GPCRs may be used in the
 CC identification of their endogenous ligands, and to screen potential GPCR
 CC agonists and antagonists for use as pharmaceutical agents. The Proteins
 CC may also be used in the study of GPCR-mediated signalling cascades, and
 CC to elucidate their precise role in normal and diseased human conditions.
 CC Nucleic acid encoding human orphan GPCRs may be used for tissue
 CC localisation expression analysis to provide information about their
 CC function in healthy and pathological states.

XX Sequence 342 AA;

Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 21; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MQAVDNLTSAAPNTISLCTRDKITQVLFPLIYTVLFGTLINGLAMRIFQIRSKSNFI 60
 QY 61 IFLKNVNTISDLMLMILTPPFKILSDAKLGTGPRTFVQVTSVIVYFTMYISISPEGLITI 120
 Db 61 IFLKNVNTISDLMLMILTPPFKILSDAKLGTGPRTFVQVTSVIVYFTMYISISPEGLITI 120
 QY 121 DRYQKTRPFPKTSNPKNLGAIIISLPMILTINQPRDGNKRCFSFLKS 180
 Db 121 DRYQKTRPFPKTSNPKNLGAIIISLPMILTINQPRDGNKRCFSFLKS 180
 QY 181 EFGLVWHEIVNVTCQVIFWIFNPLIVCYTLLTKELYRSYTRGKVPRKVNKVFI 240
 Db 181 EFGLVWHEIVNVTCQVIFWIFNPLIVCYTLLTKELYRSYTRGKVPRKVNKVFI 240
 QY 241 IIAVEFFICFVPPHFAPIPYTSLQTRDVFDCTAENTLYVKESTLWLTSLNACLDPIYFF 300
 Db 241 IIAVEFFICFVPPHFAPIPYTSLQTRDVFDCTAENTLYVKESTLWLTSLNACLDPIYFF 300
 QY 301 LCKSFRNLSLIMLKCPNSATSLISODNRKKECQGGDNEETPM 342
 Db 301 LCKSFRNLSLIMLKCPNSATSLISODNRKKECQGGDNEETPM 342

RESULT 3
 ID AAB02840 Standard; Protein: 342 AA.
 XX AAB02840;
 XX DT 22-AUG-2000 (first entry)
 XX DE Human G protein coupled receptor hCNIBs protein SEQ ID NO:34.
 XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 XX KW identification; agonist; screening; therapeutic; pharmaceutical;
 XX KW mutant.
 OS Homo sapiens.
 XX PN WO2000022131-A2.
 XX PD 20-APR-2000.
 XX PF 13-OCT-1997; 99WO-US24065.
 PR 13-OCT-1998; 98US-0170496.
 PR 12-NOV-1998; 98US-0118029.
 PR 20-NOV-1998; 98US-0109213.
 PR 27-NOV-1998; 98US-0110060.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123944.
 PR 12-MAR-1999; 99US-0123945.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123948.
 PR 12-MAR-1999; 99US-0123949.
 PR 12-MAR-1999; 99US-0123951.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-013127.
 PR 28-MAY-1999; 99US-0137131.
 PR 28-MAY-1999; 99US-0137567.
 PR 30-JUN-1999; 99US-011448.
 PR 27-AUG-1999; 99US-0151114.
 PR 03-SEP-1999; 99US-0152524.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156634.

XX PA (AREN-) ARENA PHARM INC.
 XX PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
 XX DR WPI; 2000-317986/27.
 XX N-PSDB; AAA16034.
 XX PT Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents -
 XX PS Example 1; Page 112-113; 187pp; English.
 CC The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents, AA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention.
 XX SQ Sequence 342 AA;

Query Match	Match	Score	Length
Best Local Matches	342;	100.0%;	342;
Local Similarity	100.0%;	Pred. No. 5.3e-187;	
Mismatches	0;	Mismatches 0;	
Indels	0;	Indels 0;	
Gaps	0;	Gaps 0;	

QY 1 MQAVDNLTSAAPNTISLCTRDKITQVLFPLIYTVLFGTLINGLAMRIFQIRSKSNFI 60
 Db 1 MQAVDNLTSAAPNTISLCTRDKITQVLFPLIYTVLFGTLINGLAMRIFQIRSKSNFI 60
 QY 61 IFLKNVNTISDLMLMILTPPFKILSDAKLGTGPRTFVQVTSVIVYFTMYISISPEGLITI 120
 Db 61 IFLKNVNTISDLMLMILTPPFKILSDAKLGTGPRTFVQVTSVIVYFTMYISISPEGLITI 120
 QY 121 DRYQKTRFKEKTSNPKNLGAIIISLPMILTINQPRDGNKRCFSFLKS 180
 Db 121 DRYQKTRFKEKTSNPKNLGAIIISLPMILTINQPRDGNKRCFSFLKS 180
 QY 181 EFGLVWHEIVNVTCQVIFWIFNPLIVCYTLLTKELYRSYTRGKVPRKVNKVFI 240
 Db 181 EFGLVWHEIVNVTCQVIFWIFNPLIVCYTLLTKELYRSYTRGKVPRKVNKVFI 240
 QY 241 IIAVEFFICFVPPHFAPIPYTSLQTRDVFDCTAENTLYVKESTLWLTSLNACLDPIYFF 300
 Db 241 IIAVEFFICFVPPHFAPIPYTSLQTRDVFDCTAENTLYVKESTLWLTSLNACLDPIYFF 300
 QY 301 LCKSFRNLSLIMLKCPNSATSLISODNRKKECQGGDNEETPM 342
 Db 301 LCKSFRNLSLIMLKCPNSATSLISODNRKKECQGGDNEETPM 342

RESULT 4
 ID AAY94444 standard; protein: 342 AA.
 XX DE Human 15625 receptor protein.
 XX KW Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
 XX KW glial cells; spleen; colon; liver; brain; T-cell; heart;
 XX KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
 XX KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Domain 1-25
 FT Label extracellular_domain
 FT Modified-site 6-9
 FT Label N-glycosylation

PT Misc-difference 13 /note= "encoded by ACC"
 PT Modified-site 13..16 /label= N-Glycosylation
 PT Domain - 26..302 /label= Transmembrane_domain
 PT Modified-site 39..44 /label= N-myristoylation
 PT Modified-site 121..123 /label= GPCR signal transduction site
 PT Modified-site 126..128 /label= protein_kinase_C_phosphorylation
 FT Modified-site 163..165 /label= protein_kinase_C_phosphorylation
 PT Modified-site 173..176 /label= protein_kinase_C_phosphorylation
 PT Domain 303..342 /label= Intracellular_domain
 PT Modified-site 304..305 /label= Protein_kinase_C_phosphorylation
 PT Modified-site 333..338 /label= N-myristoylation
 XX PN WO200028028-A1.
 XX PD 18-MAY-2000.
 XX PF 05-NOV-1999; 99WO-US25956.
 XX PR 06-NOV-1998; 98US-0187134.
 PR 25-AUG-1999; 99US-0332918.
 XX PA (MILLI-) MILLENNIUM PHARM INC.
 XI Glucksmann MA, Gu W, Weich NS;
 DR WPI; 2000-376543/32.
 XX N-PSDB; AAA27126.
 PT Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia -
 XX Disclosure; Page 88-89; 97pp; English.
 CC The present sequence shows the 15625 receptor protein. It is a novel G-coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues.
 CC The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein.
 CC The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia.
 XX Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 21; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5; 3e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQAVDNLTSAPGNTSLCTRDKITQVLFPFLTYLFFVGLTTLNGLAMRIFFQIRSKSNFI 60
 Db 1 MQAVDNLTSAPGNTSLCTRDKITQVLFPFLTYLFFVGLTTLNGLAMRIFFQIRSKSNFI 60

Qy 61 IFLKNTVIVSIDLMLTPEPFKILSDAKLGTCPLRTVQCVTIVYFTMYISISFLGHTI 120
 Db 61 IFLKNTVIVSIDLMLTPEPFKILSDAKLGTCPLRTVQCVTIVYFTMYISISFLGHTI 120

Qy 121 DRYOKTTTREPKTSNPKNQULGAKTLLSVVWAPMFLLSLPNMILTNRPRDKNVKKCSFLKS 180
 Db 121 DRYOKTTTREPKTSNPKNQULGAKTLLSVVWAPMFLLSLPNMILTNRPRDKNVKKCSFLKS 180

Qy 181 EFGLYWHEVNVYICQVIFWNPFLVNLIVCYLTKELYRSYTRGIGKVPRKVKVFI 240
 Db 181 EFGLYWHEVNVYICQVIFWNPFLVNLIVCYLTKELYRSYTRGIGKVPRKVKVFI 240

Qy 241 IIAVFVICTPPHFARIPTYLSOTRDYFDCTAENTLYFYKESTIWLTSINACLDPFTYF 300
 Db 241 IIAVFVICTPPHFARIPTYLSOTRDYFDCTAENTLYFYKESTIWLTSINACLDPFTYF 300

Qy 301 LCKSFRTNSLISMUKCPNATSISQDNRKKEQQGDPNEETPM 342
 Db 301 LCKSFRTNSLISMUKCPNATSISQDNRKKEQQGDPNEETPM 342

RESULT 5
 AAM79249 ID AAM79249 standard; Protein; 342 AA.
 XX AC AAM79249;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human protein SEQ ID NO 1911.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 nervous system disorder; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PN WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PP 05-FEB-2001; 2001NO-US04098
 XX PR 03-FEB-2000; 2000US-0436914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0568075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0633561.
 PR 20-OCT-2000; 2000US-0633325.
 PR 30-NOV-2000; 2000US-0728422.
 XX PA (HYSEQ -) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AU, Yang Y, Wehrman T, Goodrich R;
 XX DR WPI; 2001-476283/51.
 XX DR N-PSDB; ARK52382.

XX PT Nucleic acid encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 4310; 6221PP; English.

XX PS Claim 20; Page 4310; 6221PP; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW7833-AM8032) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibitory activity and may be useful in the diagnosis and/or treatment of cancer, arthritis, nervous system disorders, arthritis and

CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAK0020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX	Sequence	342 AA;	Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 342; Sequence	100.0%; Score 1778; DB 22; Length 342; Best Local Similarity 100.0%; Pred. No. 5.3e-18; Mismatches 0; Indels 0; Gaps 0;	PR 23-DEC-1999; PA (CORT-) COR THERAPEUTICS INC.
Qy	1	MQAVDNLTSAGNTSLCTRDYKIQVLFLIYTLEFFVGLINTGLAIIFFQRISNSNFI	60	61 IFLKNTVISLMLMILTPPKILSDAKLGTPLRPFVQCQTSWTFYFNMVISSPFLGTTI	120
Db	1	MQAVDNLTSAGNTSLCTRDYKIQVLFLIYTLEFFVGLINTGLAIIFFQRISNSNFI	60	61 IFLKNTVISLMLMILTPPKILSDAKLGTPLRPFVQCQTSWTFYFNMVISSPFLGTTI	120
Qy	121	DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180	121 DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180
Db	121	DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180	121 DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180
Qy	181	EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240	181 EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240
Db	181	EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240	181 EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240
Qy	241	IIAVFVICFVPHFARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300	241 IIAVFVICFVPHFARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300
Db	241	IIAVFVICFVPHFARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300	241 IIAVFVICFVPHFARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300
Qy	301	IACKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342	301 IACKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342
Db	301	IACKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342	301 IACKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342
DT	04-SEP-2001	(First entry)			
XX	DE	Human P2-purinergic receptor subtype, P2Y12.			
XX	ID	AAE04386 standard; Protein; 342 AA.			
XX	AC	AAE04386;			
XX	DT	04-SEP-2001 (First entry)			
XX	DE	Human P2-purinergic receptor subtype, P2Y12.			
XX	KW	Human; P2-purinergic receptor; P2Y12; cardiotropic; vasotroponic; thrombolytic; cerebroprotective; synecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic C; embolism; thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein; Gi; disseminated intravascular coagulation; thrombosis.			
XX	OS	Homo sapiens.	Location/Qualifiers		
FT	Key	27..50			
FT	Domain	/label= Transmembrane_domain_1			
FT	Domain	58..82			
FT	Domain	/label= Transmembrane_domain_2			
FT	Domain	97..121			
FT	Domain	/label= Transmembrane_domain_3			
FT	Domain	140..163			
FT	Domain	/label= Transmembrane_domain_4			
FT	Domain	189..213			
FT	Domain	/label= Transmembrane_domain_5			
FT	Domain	234..259			
FT	Domain	/label= Transmembrane_domain_6			
FT	Domain	278..303			
FT	Domain	/label= Transmembrane_domain_7			
PN	WO200146454-A1.				
XX	28-JUN-2001.				
PD	26-DEC-2000; 2000WO-US34998.				
XX	23-DEC-1999; 99US-0171622.				
PR	Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;				
XX	Hollister G;				
PA	WPI: 2001-418082/44.				
XX	N-PSSB; AAD0895.				
PT	Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications -				
XX	Example 1; Fig 5A; 108pp; English.				
PS					
XX	The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin-sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular coagulation, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic thrombocytopaenic purpura or a bleeding disorder; thrombotic and restenotic complications following angioplasty, carotid endarterectomy, CABG (coronary artery bypass graft) surgery, vascular graft surgery, stent placements or insertion of endovascular devices and prostheses. P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is human P2-purinergic receptor subtype, referred as P2Y12.				
XX	Sequence 342 AA;				
SQ	Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	MQAVDNLTSAGNTSLCTRDYKIQVLFLIYTLEFFVGLINTGLAIIFFQRISNSNFI	60	1 MQAVDNLTSAGNTSLCTRDYKIQVLFLIYTLEFFVGLINTGLAIIFFQRISNSNFI	60
Db	1	MQAVDNLTSAGNTSLCTRDYKIQVLFLIYTLEFFVGLINTGLAIIFFQRISNSNFI	60	1 MQAVDNLTSAGNTSLCTRDYKIQVLFLIYTLEFFVGLINTGLAIIFFQRISNSNFI	60
Qy	61	IFLKNTVISLMLMILTPPKILSDAKLGTPLRPFVQCQTSWTFYFNMVISSPFLGTTI	120	61 IFLKNTVISLMLMILTPPKILSDAKLGTPLRPFVQCQTSWTFYFNMVISSPFLGTTI	120
Db	61	IFLKNTVISLMLMILTPPKILSDAKLGTPLRPFVQCQTSWTFYFNMVISSPFLGTTI	120	61 IFLKNTVISLMLMILTPPKILSDAKLGTPLRPFVQCQTSWTFYFNMVISSPFLGTTI	120
Qy	121	DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180	121 DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180
Db	121	DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180	121 DRYQKTRPPTSNPKNLGAKILSVVIAWFELLSLPMMILTNRQFDKNTVKCSPLKS	180
Qy	181	EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240	181 EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240
Db	181	EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240	181 EFGLYWHEITVNYICCVIWFNLFIVCYTLITKELYRSYVTRGVYKPVKRVNKFV	240
Qy	241	IIAVPICFYPFHARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300	241 IIAVPICFYPFHARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300
Db	241	IIAVPICFYPFHARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300	241 IIAVPICFYPFHARIPIYTSQTRDVFCTAENTLTYKESTIWLTSLNACLDPFYFF	300
Qy	301	LCKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342	301 LCKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342
Db	301	LCKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342	301 LCKSFRNLSIISMILKCPNSATSLQSQNRRKEQDGDPNEETPM	342

RESULT 7
 ABP9608
 ID ABP95608 Standard; Protein; 342 AA.
 XX
 AC ABP95608;
 XX
 DT 06-MAR-2003 (first entry)
 DE Human GPCR polypeptide SEQ ID NO 26.
 XX
 KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory; taste; fragrance; receptor; drug development; gustatory; table; fragrance; receptor.
 XX
 OS Homo sapiens.
 PN WO200216548-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-IB01446.
 XX
 PR 04-AUG-2000; 2000JP-0237818.
 PR 13-FEB-2001; 2001JP-0034434.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Haga T, Takeda S, Mitaku S;
 XX
 DR WPI; 2002-304118/34.
 DR ABZ42882.
 XX
 PT Database global search for G protein-coupled receptors, proteins and encoded genes for studying in vivo signal transduction mechanism and identifying targets for drug development -
 XX
 PS SEQ ID NO 26; 97pp + Sequence Listing; Japanese.
 XX
 CC The invention relates to a method for screening G protein-coupled receptor (GPCR) Genes (AB242870-Ab243216) and/or GPCR proteins (ABP9596-ABP95942) by extracting open-reading frames containing 6-8 transmembrane domains with 250-1000 amino acid residues to give a gene homologous with a known GPCR Gene. The receptor proteins and encoded genes are useful for studying in vivo signal transduction mechanism and identifying targets for drug development e.g. based on olfactory and gustatory receptors in form of agonists and antagonists by screening intrinsic and extrinsic ligands as bitter taste inhibitors, taste enhancers and fragrance improvers.
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 342 AA;

Qy 241 IIAVPPICCPFPARIPIVTLISQTRDPCDTAENTLYVKESTLWLTSLNACLDPFIVF 300
 ABP9608
 ID ABP95608 Standard; Protein; 342 AA.
 Db 241 IIAVPPICCPFPARIPIVTLISQTRDPCDTAENTLYVKESTLWLTSLNACLDPFIVF 300
 AC
 301 LCKSPRNSLISMKCPNSATSLQDNKKEQDGDPNEETPM 342
 Qy 301 LCKSPRNSLISMKCPNSATSLQDNKKEQDGDPNEETPM 342
 Db 301 LCKSPRNSLISMKCPNSATSLQDNKKEQDGDPNEETPM 342

RESULT 8
 ABB77868
 ID ABB77868 standard; Protein; 342 AA.
 XX
 AC ABB77868;
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DB Amino acid sequence of human ADP receptor P2TAC protein.
 XX
 KW Human; ADP receptor; P2TAC; antiplatelet agent; thrombotic disease; ischaemic disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200236631-A1.
 XX
 PD 10-MAY-2002.
 XX
 PR 31-OCT-2001; 2001WO-JP09534.
 PR 01-NOV-2000; 2000JP-0334721.
 PR 11-JAN-2001; 2001JP-0003577.
 XX
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 XX
 PI Takasaki J, Matsumoto M, Kamohara M, Saito T, Ohishi T, Soga T;
 DR WPI; 2002-519336/55.
 DR AB59205.
 XX
 PT Method for screening anti-platelet agents with human ADP receptor P2TAC protein, its functional equivalent, or its homologous protein, as tool, for treating e.g. thrombotic or ischaemic diseases -
 PT
 XX
 PS Page 48-49; 56pp; Japanese.
 XX
 CC The present sequence represents a human ADP receptor P2TAC protein. It is used as a screening tool for screening for antiplatelet agents. The method is used for screening for antiplatelet agents, which can then be used for treating e.g. thrombotic or ischaemic diseases.
 CC
 XX
 SQ Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 23; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5_3e-187; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MOAVDNITSAGNTSICTRDYKITOVLFPFLPLTYLFFVGLITNGLMRIFFOQRSKSNFI 60
 Db 1 MOAVDNITSAGNTSICTRDYKITOVLFPFLPLTYLFFVGLITNGLMRIFFOQRSKSNFI 60
 Qy 61 IFLKNTVISDLIMLITFPFKILSDAKLGTLGTLRPLRTFCQTSVITYFTMVISPLGLITI 120
 Db 61 IFLKNTVISDLIMLITFPFKILSDAKLGTLGTLRPLRTFCQTSVITYFTMVISPLGLITI 120
 Qy 121 DRYQKTRPFTSNPQLLGKILSVIWAAMPFLSLPMLNITRQPRDKNNKKCSPLKS 180
 Db 121 DRYQKTRPFTSNPQLLGKILSVIWAAMPFLSLPMLNITRQPRDKNNKKCSPLKS 180
 Qy 181 EFGLVWHEIVNYICQVIFWNFLIVCYTLLITKELYRSVTRGVGKVRPKCIVNKVYFI 240
 Db 181 EFGLVWHEIVNYICQVIFWNFLIVCYTLLITKELYRSVTRGVGKVRPKCIVNKVYFI 240
 Qy 181 EFGLVWHEIVNYICQVIFWNFLIVCYTLLITKELYRSVTRGVGKVRPKCIVNKVYFI 240
 Db 181 EFGLVWHEIVNYICQVIFWNFLIVCYTLLITKELYRSVTRGVGKVRPKCIVNKVYFI 240

QY 241 IIAVEFICVPFHAFIPIVTLTSQTRDFCTAENTLTVKESTLWLTSLNACLDPTIYFF 300
 Db 241 IIAVEFICVPFHAFIPIVTLTSQTRDFCTAENTLTVKESTLWLTSLNACLDPTIYFF 300
 301 LCKSFRNSLISMKCPNSATSLSDNRKEQDGDPNEETPM 342
 Db 301 LCKSFRNSLISMKCPNSATSLSDNRKEQDGDPNEETPM 342

RESULT 9
 AAU80164 AAU80164 Standard; Protein: 342 AA.

XX Human; ADP-glucose; receptor; G protein-coupled receptor;
 XX agonist; antagonist; cardiovascular function disorder; vasorelaxation;
 XX ischaemia; angina pectoris; gastrointestinal disorder; diarrhoea;
 XX immunodeficiency disorder; autoimmune disorder;
 XX rheumatoid arthritis; bacterial infection; viral infection;
 XX fungal infection; protozoal infection; respiratory disorder; asthma;
 XX kidney disorder; glomerulonephritis; hepatobiliary disorder; cirrhosis;
 XX endocrine disorder; adrenal dysfunction; musculoskeletal disorder;
 XX osteoporosis; nervous system disorder; Alzheimer's disease;
 XX psychotropic disorder; depression; cancer; pain; glycogen storage disease;
 XX disorder of body weight; AIDS; acquired immunodeficiency syndrome;
 XX chromosome 3; Usher's syndrome type 3.

OS Homo sapiens.

PN WO200224942-A2.

PD 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US29523.

XX 20-SEP-2000; 2000US-234025P.

PR 09-FEB-2001; 2001US-0790576.

XX (REBG) UNIV CALIFORNIA.

PI Civelli O, Nothacker H, Wang Z, Reinscheid R;

DR WPI: 2002-383195/41.

XX Identifying an agonist, antagonist or ligand of an ADP-Glucose receptor, for treating cardiovascular, renal, gastrointestinal, kidney, endocrine, immune disorders, and bacterial, viral, protozoal or fungal infections.

PS Claim 3; Fig 1; 86pp; English.

CC The ant/agonists are useful therapeutically for preventing or ameliorating conditions associated with the receptor such as cardiovascular disorders (e.g. ischaemia, hypertension, hypotension, angina pectoris, myocardial infarction, stroke, congestive heart failure, shock, erectile dysfunction, orthostatic intolerance and migraine), gastrointestinal disorders (e.g. diarrhoea, gastritis, inflammatory bowel disease), immune disorders (e.g. immunodeficiency disorders, autoimmune disorders, rheumatoid arthritis), infections (e.g. asthma, pneumonia, bronchitis) or virus, respiratory disorders (e.g. jaundice, cirrhosis, hepatitis), hepatic disorders (e.g. pituitary, thyroid or adrenal dysfunction), endocrine disorders (e.g. osteoporosis, muscular dystrophies), nervous system disorders (e.g. Parkinson's and Alzheimer's disease), psychiatric disorders (e.g. depression, anxiety, schizophrenia), pain, glycogen storage diseases and disorders of body weight (e.g. as a result of cancer or AIDS, acquired immunodeficiency syndrome). The gene for the ADP-G receptor is located on chromosome 3 in a region associated with Usher syndrome type 3 (progressive hearing loss). The ligand is useful therapeutically, in detecting normal or abnormal expression of the receptor in an isolated sample or in vivo diagnostic imaging procedures, and targeting specifically a diagnostic group to cells and tissues that express the receptor. The present sequence represents the ADP-G receptor.

XX Sequence 342 AA;

SQ Query Match 100.0%; Score 1778; DB 23; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5; 3e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MOAVDNLTASAGNTSLCIRDYKITQVLEPLLYLTFYFFGLTINGLAMRIFTQIRSKNF 60
 Db 1 MOAVDNLTASAGNTSLCIRDYKTQVLEPLLYLTFYFFGLTINGLAMRIFTQIRSKNF 60
 Qy 61 IFLKNTVSPDMLMTEPKTISPKNLGAKILSVVIAWFMLSLPMILTNQPDKNVKCSFKS 120
 Db 61 IFLKNTVSPDMLMTEPKTISPKNLGAKILSVVIAWFMLSLPMILTNQPDKNVKCSFKS 120
 Qy 121 DRYQKTTTPKTSNPKNLGAKILSVVIAWFMLSLPMILTNQPDKNVKCSFKS 180
 Db 121 DRYQKTTTPKTSNPKNLGAKILSVVIAWFMLSLPMILTNQPDKNVKCSFKS 180
 Qy 181 EFGLVWHEIVNYICQVTFINFLIVTCYLLKELYSYVTRGVGVPRKCVNVKF 240
 Db 181 EFGLVWHEIVNYICQVTFINFLIVTCYLLKELYSYVTRGVGVPRKCVNVKF 240
 Qy 241 IIAVEFICVPFHAFIPIVTLTSQRDVFECTAENTLTVKESTLWLTSLNACLDPTIYFF 300
 Db 241 IIAVEFICVPFHAFIPIVTLTSQRDVFECTAENTLTVKESTLWLTSLNACLDPTIYFF 300

RESULT 10
 AAM43353 standard; Protein: 342 AA.

XX AAM43353;

AC AAM43353;

DT 25-APR-2002 (first entry)

DB Human G protein-coupled receptor, IGPR17.

XX Human; G protein-coupled receptor; IGcR17; analgesic; neuroleptic; tranquiliser; anti-parkinsonian; neuroprotective; nootropic; anti-inflammatory; anticonvulsant; metabolic; anorectic; anabolic; antiasthmatic; antiallergic; antiarthritic; antidiarrheic; otorcopathic; antiasthmatic; anti-allergic; gene therapy; psychiatric disorder; immunosuppressive; movement dysunction; schizophrenia; central nervous system disorder;

KW	multiple sclerosis; Alzheimer's disease; kidney disease; obesity;	Qy	301 LCKSPRNSLISMLKCPSNATSLSODNRKKEQDGDDPNEETPM	342
KW	gastrointestinal disorder; osteoporosis; infection;	Db	301 LCKSPRNSLISMLKCPSNATSLSODNRKKEQDGDDPNEETPM	342
XX	gynecological disorder; receptor.			
OS	Homo sapiens.			
PN	WO200202599-A2.			
XX	PD 10-JAN-2002.			
XX	PP 02-JUL-2001; 2001WO-EP07532.			
XX	PR 30-JUN-2000; 2000US-215759P.			
XX	PA (INGE-) INGENIUM PHARM AG.			
XX	PI Wattier F, Wattler S, Trommler P, Nehls MC;			
XX	PT New human or mouse G protein-coupled receptor protein, IGPcR17, useful for diagnosis, prevention, amelioration or treatment of central nervous system disorders such as Tourette's syndrome, Parkinson's disease and pain -			
XX	PS Claim 8; Fig 2; 71pp; English.			
XX	CC The present sequence is the protein sequence for human G protein-coupled receptor (GPCR) protein, IGPcR17. The coding sequence for IGPcR17 is useful in gene therapy for prevention, amelioration or treatment of diseases characterized by aberrant expression or activity of IGPcR17, where the disease is a psychiatric or central nervous system (CNS) disorder associated with signal processing in CNS such as learning and memory disorders, movement dysfunctions, tremor, Tourette's syndrome, Huntington's disease, dyskinetias, dystonia, pain and spasms. In addition, IGPcR17 and its coding sequence are useful in diagnosis, prevention, amelioration or treatment of disease associated with signal processing in CNS, schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia, anorexia, kidney diseases such as renal failure, obesity, gastrinoma, gastrointestinal disorders such as irritable bowel syndrome (IBS), diarrhoea, motility disorders and conditions of delayed gastric emptying, osteoporosis, infections such as bacterial, fungal, protozoal and viral infections, asthma, allergy, arthritis, sepsis and gynecological disorders.			
XX	QQ Sequence 342 AA;			
Qy	Query Match 100.0%; Score 1778; DB 23; Length 342; Best Local Similarity 100.0%; Pred. No. 5_36-187; Mismatches 0; Indels 0; Gaps 0;			
Db	Matches 342; Conservative 0; MisMatches 0; Indels 0; Gaps 0;			
Qy	1 M QDAVNNTSAPENTSLCTRDKITKTOVLFPPLIYTIVLFFVGLITNGAMRIFQFTRSKSNFI 60			
Db	1 M QDAVNNTSAPENTSLCTRDKITKTOVLFPPLIYTIVLFFVGLITNGAMRIFQFTRSKSNFI 60			
Qy	61 IPIKNNTVSDLMILTEPFKLSDAKIGTPGIRTFVQTVSIYFTMYSISPIGLTI 120			
Db	61 IPIKNNTVSDLMILTEPFKLSDAKIGTPGIRTFVQTVSIYFTMYSISPIGLTI 120			
Qy	121 DRYQKTRRPFKTSNPQNLGAKILSTVIAFMFLSLPNMILTNQPRDKNKKCSFLKS 180			
Db	121 DRYQKTRRPFKTSNPQNLGAKILSTVIAFMFLSLPNMILTNQPRDKNKKCSFLKS 180			
Qy	181 EFLFLWHEIVNYICQVIFWNLIVCYTILTKELYRSVTRGVYKPRKCNVYKI 240			
Db	181 EFLFLWHEIVNYICQVIFWNLIVCYTILTKELYRSVTRGVYKPRKCNVYKI 240			
Qy	241 IIAVFFICFVPPFHARIPTYLSQTRDVFDCTAENTLYVKEESTLWLTSLNACLDPPFYF 300			
Db	241 IIAVFFICFVPPFHARIPTYLSQTRDVFDCTAENTLYVKEESTLWLTSLNACLDPPFYF 300			

QY 1 M Q A V D N I T S A P G N T S L C P R D Y K I T Q V I F P L I Y T V L F P V G L I N T G L A M R I P Q I R S K S N F I 60
 Db 1 M Q A V D N I T S A P G N T S L C P R D Y K I T Q V I F P L I Y T V L F P V G L I N T G L A M R I P Q I R S K S N F I 60
 QY 61 I F L K N T V I S D L M I L T E P P K I L S D A K L G T G P A R T F V C O V T S V I F Y F M Y I S I S P L G I T I 120
 Db 61 I F L K N T V I S D L M I L T E P P K I L S D A K L G T G P A R T F V C O V T S V I F Y F M Y I S I S P L G I T I 120
 QY 121 D R Y Q T K T R P K T S M P K N U L G A K I L S V V I W A M P I L S L P N M I T N Q P R D K N T K C S P L K S 180
 Db 121 D R Y Q T K T R P K T S M P K N U L G A K I L S V V I W A M P I L S L P N M I T N Q P R D K N T K C S P L K S 180
 QY 181 E F G L Y W H E V N Y I C Q V I W N I F L I V I C Y T L I K E L Y R S Y V T R G V K P R K V N V K V F I 240
 Db 181 E F G L Y W H E V N Y I C Q V I W N I F L I V I C Y T L I K E L Y R S Y V T R G V K P R K V N V K V F I 240
 QY 241 I I A V F F C V P F H P A R I P Y T S L Q T R D V D C T A E N T L F Y V K E S T L W L T S L N A C L D P F I Y F 300
 Db 241 I I A V F F C V P F H P A R I P Y T S L Q T R D V D C T A E N T L F Y V K E S T L W L T S L N A C L D P F I Y F 300
 QY 301 L C K S F R N S L I S M I . K C P N S A T S I S Q D N R K E Q D G D P N E E T P M 342
 Db 301 L C K S F R N S L I S M I . K C P N S A T S I S Q D N R K E Q D G D P N E E T P M 342

RESULT 12
 ID AAC80236 Standard; Protein: 342 AA.

AC AAC80236;

XX DT 24-JAN-2002 (first entry)

DE Human PAFR3 protein.

XX KW Platelet activating factor receptor; human; chromosome 3;

KW thrombocyte activation; hypotension; vascular permeability;
 KW bronchoconstriction; transgenic animal; knockout animal.
 XX OS Homo sapiens.

XX PN DE10020073-A1.

XX PD 25-OCT-2001.

XX PP 22-APR-2000; 2000DE-1020073.

XX PR 22-APR-2000; 2000DE-1020073.

XX PA (BRUE/) BRUESS M.

PA (BOEN/) BOENISCH H.

PI PIERS M.

PI Boenisch H;

XX DR WPI:2002-027296/04.

DR N-PSDB; AAI68802, AAI68803.

XX PS Disclosure: Page 4; 6pp; German.

PT New human platelet-activating factor (PAF) receptor-3 gene, useful for
 PT diagnosis and treatment of PAF-related diseases -

XX Disclosure: Page 4; 6pp; German.

XX PT

CC This invention describes a novel human platelet-activating factor (PAF)
 CC receptor-3 (PAFR-3) gene (I). The protein encoded by (I) probably
 CC modulates the activity of PAF, which is involved in many
 CC (patho)physiological processes, e.g., thromocyte activation,
 CC hypotension, increased vascular permeability, bronchoconstriction etc.
 CC (I), and derived (anti)sense oligonucleotides, are useful in the
 CC treatment and diagnosis of (I)-related diseases; for producing
 CC transgenic/knockout animals, and for recombinant expression of the
 CC protein (I) that it encodes. (II) is useful in ligand-binding studies
 CC and screening assays, also for treatment and diagnosis of (II)-related

CC diseases. This sequence represents the human platelet-activating
 CC factor receptor (PAFR-3) protein described in the invention.

XX SQ Sequence 342 AA;

QY Query Match 100.0%; Score 1778; DB 23; Length 342;

Db Best Local Similarity 100.0%; Pred. No. 5.3e-187;

Db Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 M Q A V D N I T S A P G N T S L C P R D Y K I T Q V I F P L I Y T V L F P V G L I N T G L A M R I P Q I R S K S N F I 60

Db 1 M Q A V D N I T S A P G N T S L C P R D Y K I T Q V I F P L I Y T V L F P V G L I N T G L A M R I P Q I R S K S N F I 60

Qy 61 I F L K N T V I S D L M I L T E P P K I L S D A K L G T G P A R T F V C O V T S V I F Y F M Y I S I S P L G I T I 120

Db 61 I F L K N T V I S D L M I L T E P P K I L S D A K L G T G P A R T F V C O V T S V I F Y F M Y I S I S P L G I T I 120

Qy 121 D R Y Q T K T R P K T S M P K N U L G A K I L S V V I W A M P I L S L P N M I T N Q P R D K N T K C S P L K S 180

Db 121 D R Y Q T K T R P K T S M P K N U L G A K I L S V V I W A M P I L S L P N M I T N Q P R D K N T K C S P L K S 180

Qy 181 E F G L Y W H E V N Y I C Q V I W N I F L I V I C Y T L I K E L Y R S Y V T R G V K P R K V N V K V F I 240

Db 181 E F G L Y W H E V N Y I C Q V I W N I F L I V I C Y T L I K E L Y R S Y V T R G V K P R K V N V K V F I 240

Qy 241 I I A V F F C V P F H P A R I P Y T S L Q T R D V D C T A E N T L F Y V K E S T L W L T S L N A C L D P F I Y F 300

Db 241 I I A V F F C V P F H P A R I P Y T S L Q T R D V D C T A E N T L F Y V K E S T L W L T S L N A C L D P F I Y F 300

Qy 301 L C K S F R N S L I S M I . K C P N S A T S I S Q D N R K E Q D G D P N E E T P M 342

Db 301 L C K S F R N S L I S M I . K C P N S A T S I S Q D N R K E Q D G D P N E E T P M 342

RESULT 13

ABPP1734

ID ABPP1734 standard; Protein: 342 AA.

XX AC ABPP1734;

XX DT 04-MAR-2003 (first entry)

XX DE ABPP1734

XX ID ABPP1734 standard; Protein: 342 AA.

XX AC ABPP1734;

XX DT 04-MAR-2003 (first entry)

XX DE Human PY12 platelet ADP receptor protein SEQ ID NO:643.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

XX KW G protein-coupled receptor modulator; antibody; immune-related disease;

XX KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

XX KW immunological-related cell proliferative disease; autoimmune disease;

XX KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

XX KW osteoporosis; cardiomopathy; inflammation; Crohn's disease; diabetes;

XX KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

XX KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

XX KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

XX KW hypertension; hypertension; renal disorder; rheumatoid arthritis; trauma;

XX KW ulcer.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PR 19-DEC-2001; 2001WO-US50107.

XX PR 19-DEC-2000; 2000US-257144B.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burner GC, Roush CL, Brown JP;

XX DR WPI: 2003-046718/04.

XX N-PDB; AB24580.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases

Disclosure: Fig 1; 523pp; English.

CC The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP82619) of 12-24 amino
 CC acids. Also described is (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoporosis, ostearthritis, cancer, cardiomopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders or rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ4223 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 24; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQDNLTSAGNTSICTRDYKITYLFPFLTYVLFPEVLITGLANLIFQFRSKSNFI 60

Db 1 MAQDNLTSAGNTSICTRDYKITYLFPFLTYVLFPEVLITGLANLIFQFRSKSNFI 60

Qy 61 IFLKNTVISDLMILTFPPFKLSDAKLGTPLRITFVQCVTSIFYFTNYNISISFLGLHTI 120

Db 61 IFLKNTVISDLMILTFPPFKLSDAKLGTPLRITFVQCVTSIFYFTNYNISISFLGLHTI 120

Qy 121 DRYQKTRPFTSNPNKLIGRKILSVVAFMFLISLPMLNLTRQPDKNCKCSPLKS 180

Db 121 DRYQKTRPFTSNPNKLIGRKILSVVAFMFLISLPMLNLTRQPDKNCKCSPLKS 180

Qy 181 EFGLYWHEIVNYICQVIFWINFLLIVTCVTLITKBLYSYRTRGVGKVPRKCVNKFVI 240

Db 181 EFGLYWHEIVNYICQVIFWINFLLIVTCVTLITKBLYSYRTRGVGKVPRKCVNKFVI 240

Qy 241 IIAVFFFCVPPHFAPIPYTISQTRDFCTAENTLYKESTIWLTSLNACLDPPYFF 300

Db 241 IIAVFFFCVPPHFAPIPYTISQTRDFCTAENTLYKESTIWLTSLNACLDPPYFF 300

Qy 301 LCKSFANSLSMLKCPCNSATLSQDNRKKEQDGDPNEETPM 342

Db 301 LCKSFANSLSMLKCPCNSATLSQDNRKKEQDGDPNEETPM 342

RESULT 14.

AY94445 standard; Protein: 342 AA.

XX AC AAY94445;

XX DT 21-AUG-2000 (first entry)

Macaque ortholog of human 15625 receptor protein.

XX Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
 XX Glial cells; spleen; colon; liver; brain; T-cell; heart;
 XX red cell; thymus; B-cell; Pancreas; disorder; chromosome 3;
 XX anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
 XX OS Macaca sp.
 XX PN WO200028028-A1.
 XX PD 18-MAY-2000.
 XX PF 05-NOV-1999; 99W0-US25956.
 XX PR 06-NOV-1998; 98US-0187134.
 XX PR 25-AUG-1999; 99US-0384918.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PA Glucksmann MA, Gu W, Weich NS;
 XX PI DR 2000-376543/32.
 XX DR N-PSDB; AAA7127.

Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia Disclosure; Page 90-92; 97pp; English.

The 15625 receptor protein is a novel G-coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein. The 15625 receptor protein polymucleotides are useful for generating probes, primers and antisense constructs. The polymucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polymucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia. The present sequence is the macaque ortholog of the human 15625 receptor protein.

Sequence 342 AA;

Query Match 98.3%; Score 1748; DB 21; Length 342;
 Best Local Similarity 98.0%; Pred. No. 1.1e-183;
 Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAQDNLTSAGNTSICTRDYKITYLFPFLTYVLFPEVLITGLANLIFQFRSKSNFI 60

Db 1 MAQDNLTSAGNTSICTRDYKITYLFPFLTYVLFPEVLITGLANLIFQFRSKSNFI 60

Qy 61 IFLKNTVISDLMILTFPPFKLSDAKLGTPLRITFVQCVTSIFYFTNYNISISFLGLHTI 120

Db 61 IFLKNTVISDLMILTFPPFKLSDAKLGTPLRITFVQCVTSIFYFTNYNISISFLGLHTI 120

Qy 121 DRYQKTRPFTSNPNKLIGRKILSVVAFMFLISLPMLNLTRQPDKNCKCSPLKS 180

Db 121 DRYQKTRPFTSNPNKLIGRKILSVVAFMFLISLPMLNLTRQPDKNCKCSPLKS 180

Qy 181 EFGLYWHEIVNYICQVIFWINFLLIVTCVTLITKBLYSYRTRGVGKVPRKCVNKFVI 240

Db 181 EFGLYWHEIVNYICQVIFWINFLLIVTCVTLITKBLYSYRTRGVGKVPRKCVNKFVI 240

Qy 241 IIAVFFFCVPPHFAPIPYTISQTRDFCTAENTLYKESTIWLTSLNACLDPPYFF 300

Db 241 IIAVFFFCVPPHFAPIPYTISQTRDFCTAENTLYKESTIWLTSLNACLDPPYFF 300

Qy 301 LCKSFANSLSMLKCPCNSATLSQDNRKKEQDGDPNEETPM 342

Db 301 LCKSFANSLSMLKCPCNSATLSQDNRKKEQDGDPNEETPM 342

RESULT 14.

AY94445

XX AC AAY94445;

XX DT 21-AUG-2000 (first entry)

DE

Db 301 LCKSFRNSLISMLKCPNSATSQSDNRKKEQDDPNEETPM 342

RESULT 15

AAE03385 ID AAE04385 Standard; protein; 315 AA.

AC AAE04385;

XX XX 04-SEP-2001 (first entry)

XX DE Human P2-purinergic receptor subtype, P2Y12 protein fragment.

XX Human; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein; Gi; disseminated intravascular coagulation; thrombosis.

XX OS Homo sapiens.

XX PN WO200146454-A1.

XX PD 28-JUN-2001.

XX PP 26-DEC-2000; 2000WO-US39998.

XX PR 23-DEC-1999; 99US-0171622.

XX PA (CORT-) COR THERAPEUTICS INC.

XX PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

PI Hollópeter, G;

XX PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications -

XX Example 1; Page 84-85; 108PP; English.

XX PT The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed selectively in the Platelets and brain, and couples to a Pertussis toxin-sensitive G protein (G_i). The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, preclampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic and thrombocytopaenic purpura or a bleeding disorder; thrombotic and restenotic complications following angioplasty, carotid endarterectomy, post CABG (coronary artery bypass graft) surgery, vascular graft surgery, stent placement or insertion of endovascular devices and protheses.

CC P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is a fragment of human P2-purinergic receptor subtype, referred as P2Y12.

XX SQ Sequence 315 AA;

Query Match 91.9%; Score 1634; DB 22; Length 315;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Page 2

Y	Y	61	IFLQNTVTPDLMITFPFKILSDAKLGTLGTLRVCQTVSIFTMYSISFGLITI	120
O	O	61	IFLQNTVSPDLMITFPFKILSDAKLGTLGTLRVCQTVSIFTMYSISFGLITI	120
Y	O	121	DRYQKTRPFTSNPKNLGAKILSVVIAFMFLSLPNMLTNRQFDKVKCFSFLKS	180
O	O	121	DRYQKTRPFTSNPKNLGAKILSVVIAFMFLSLPNMLTNRQFDKVKCFSFLKS	180
V	V	181	EFGLVWHEIINYICQVIFWINFLLITKELYSTYRCYCYLITKELYSTYRCY	240
O	O	181	EFGLVWHEIINYICQVIFWINFLLITKELYSTYRCYCYLITKELYSTYRCY	240
Y	O	241	IIAVERFICRYFEPHARIPYLTQSDFCTAENTLFYVTESTLNITSLNACLDPIYFF	300
O	O	241	IIAVERFICRYFEPHARIPYLTQSDFCTAENTLFYVTESTLNITSLNACLDPIYFF	300
Y	O	301	LCKSPRNSLISMKCPENSATSLSONRKKEODGDPNEETPM	342
O	O	301	LCKSPRNSLISMKCPENSATSLSONRKKEODGGDNNEETPM	342
RESULT 2				
P	P	8BZV8	PRELIMINARY;	PRY; 347 AA.
D	D	QBBZV8	PRELIMINARY;	PRY; 347 AA.
C	C	QBBZV8;		
C	C	01-MAR-2003 (TREMBLrel. 23, Created)		
T	T	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
T	T	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
B	B	P2Y12 platelet ADP receptor homolog.		
S	S	Mus musculus (Musce).		
S	S	Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
N	N	[1] NCBI TaxID=10090;		
X	X	SEQUENCE FROM N.A.		
X	X	STRAIN=C57BL/6J; TISSUE=Colon;		
X	X	MEDLINE=22354683; PubMed=12466851;		
A	A	The FANTOM Consortium,		
A	A	The RIKEN Genome Exploration Research Group Phase I & II Team;		
A	A	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";		
T	T	EMBL: AK033448; BAC8294.1; -;		
R	R	EMBL: AK033448; BAC8294.1; -;		
L	L	EMBL: AK033448; BAC8294.1; -;		
Q	Q	SEQUENCE 347 AA; 39430 MW; F114688377FE225F1 CRC64;		
Q	Q	Query Match 87.1%; Score 1548.5; DB 11; Length 347;		
Q	Q	Best Local Similarity 88.4%; Pred. No. 7.9e-124;		
Q	Q	Matches 298; Conservative 16; Mismatches 22; Indels 1; Gaps 1		
Y	Y	6 NLTSAAGNTSLCTRDYKITQLFPLLYTIVLFFGGLITGLANRIFQRSKSNFELIFRN .65		
b	b	12 NTTFSPSTTSLCTRDYKITQLFPLLYTIVLFFGGLITGLANRIFQRSKSNFELIFRN .71		
Y	Y	66 TVISDLMLITSPFKILSDAKLGTLGTLRVCQTVSIFTMYSISFGLITDYQK 125		
b	b	72 TVISDLMLITSPFKILSDAKLGTLGTLRVCQTVSIFTMYSISFGLITDYQK 131		
Y	Y	126 TTRPFKTSNPKNLGAKILSVVIAFMFLSLPNMLTNRQFDKVKCFSFLKSF 185		
b	b	132 TTRPFKTSNPKNLGAKILSVVIAFMFLSLPNMLTNRQFDKVKCFSFLKSF 191		
Y	Y	186 WHEIVNTVICQVIFWINFLLITKELYSTYRCYCYLITKELYSTYRCY		
b	b	192 WHEIVNTVICQVIFWINFLLITKELYSTYRCYCYLITKELYSTYRCY		
Y	Y	246 FICFVPPHFARIPIYTLSQTRDFCTAENTLFYVTESTLNITSLNACLDPIYFFFLCKSF 305		
b	b	252 FICFVPPHFARIPIYTLSQTRAVPCSAINTLFYVTESTLNITSLNACLDPIYFFFLCKSF 311		
Y	Y	306 RNLSLISMKCPNGSATSLSONRKKEODGDPNEETPM 342		
b	b	312 RNSTUTSMRCSNS TSTSGTNKKGEGEBSPEETPM 347		

RESULT 4

Q8TDT7	PRELIMINARY;	PRT;	352 AA.
QB1UTS			
AC	Q8TDT7;		
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Hypothetical protein (Fragment).		
OS	<i>Homo sapiens</i> (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CX	NCBI TaxID=9606;		
BN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=brain;		
RA	Strausberg R;		
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJU databases.		
DR	EMBL; BC041116; AAH4116.1; -.		
KW	Hypothetical protein.		
FT	NON_TER		
SEQUENCE	352 AA;		
Qy	197 IFWINFLIVTYCYTLITKELYRSYVRTRGVGGKVPRKKVNVKPVIIIAVFFICVFPEHFAF 256		
Db	195 IFWTVMLVTVIARKVDSRKSNSKRKNKLEGGKVFFVVAFFPFVCFAPFHFAF 254		
Qy	257 IPYTLISQTRVEDCTAENTLYFVKESTIWLTSNACUDPFIFYFLCKSFNRSLISMUKCP 316		
Db	255 VPYTHSQTNRKTDCLQNQFLIAKEETITLELAATNICMDPLIXIFLCKKPTERLPCMQ-G 312		
Qy	317 NSATLSQDNRKKEQD 332		
Db	332 RKTASSQENHSSQTD 347		

RESULT 5

Q8TDT7	PRELIMINARY;	PRT;	333 AA.
ID	Q8TDT7;		
AC	Q8TDT7;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Putative G-protein coupled receptor.		

GN GPCR.
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takeda S., Kadowaki S., Haga T., Takaezu H., Mitaku S.;
 RA "Identification of G protein-coupled receptor genes from the human genome sequence";
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJU databases.
 RL InterPro; IP0000276; GPCR_Rhodopsin.
 DR InterPro; AB083597; BAA89310.1;
 DR Pfam; PF00001; 7TM_1; 1.
 DR PROSITE; PS00337; _G_PROTEIN_RECGBP_F1_1; 1.
 DR PROSITE; PS05262; _G_PROTEIN_RECGBP_F1_2; 1.
 DR Receptor.
 SQ SEQUENCE 333 AA; 38409 MW; 3P88ETEACB95428F CRC64;
 Query Match 46.3%; Score 823; DB 4; Length 333;
 Best Local Similarity 48.7%; Pred. No. 3. 6e-62;
 Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;
 Qy 177 CTRDKITQVLFPLIYTVLFFVGLLTINGLMARIFFQIRSKSNFELFKNTVSDILMILT 76
 Db 15 CPDRTRIVQLVPALYTVLFFVGLLTINGLMARIFFQIRSKSNFELFKNTVSDILMILT 74
 Qy 77 FPFKILSDAKLGGPLRTRVQVTFQVTSVIFYFTMYSISIFLGLITDRYQTKTRPFKTSNPK 136
 Db 75 LPFKILSDHLPAPQLRATVCRSSVIVETYVFGVILGLAFDRFKIKIPLRNFLK 134
 Qy 137 NLGAKILSVVIAWMFLISLPNMILTRQPDKNTVKCSPLKFSEGLVWHETVNYICQV 196
 Db 135 KPVFAKTVSIFINWFLFFFSLPTNLTSNKEATPSVTKCSASLGKPLGKWHQVNNTICQF 194
 Qy 197 IFWNFLIVTYCYTLITKELYRSYVRTRGVGGKVPRKKVNVKPVIIAVFFICVFPEHFAF 256
 Db 195 IFWTFLMLVTVIARKVDSRKSNSKRKNKLEGGKVFFVVAFFPFVCFAPFHFAF 254
 Qy 197 IPYTLISQTRVEDCTAENTLYFVKESTIWLTSNACUDPFIFYFLCKSFNRSLISMUKCP 316
 Db 255 VPYTHSQTNRKTDCLQNQFLIAKEETITLELAATNICMDPLIXIFLCKKPTERLPCMQ-G 312
 RESULT 6
 Q9DBT2 PRELIMINARY; PRT; 337 AA.
 ID Q9DBT2 PRELIMINARY;
 AC Q9DBT2; PRELIMINARY;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DB 2010001LOGRIK Protein.
 QPR86 OR 2010001LOGRIK.
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurograthi; Murinae; Mus.
 OC NCBI TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=21:085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyoasa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gojobori T., Bonci H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda T., Asburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RESULT 9

Q8IYT7 PRELIMINARY; PRT; 338 AA.

AC Q8IYT7; ID Q8IYT7; DR 01-MAR-2003 (TREMBLrel. 23, Created) 01-MAR-2003 (TREMBLrel. 23, Last sequence update) 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE G protein-coupled receptor 105.

OS Homo sapiens (Human); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;

RN [1] PREQUENCE FROM N.A.

RC Strasbourg R.; RA Submitted (JUJ-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BCO4989; AAH34989.1; DR

SEQUENCE 338 AA; 38972 MW; 8871408E2F392DEB CRC64;

Query Match Score 77%; DB 4; Length 338; Best Local Similarity 47.5%; Pred. No. 8e-58; Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

Qy 6 NLTSAGNTSLTRKYLPIKLSLAKLGTGPLRFLFCVQTVSIFYFTMVISFLGLITIDRYQ 125 TTRPEKTSNPKNLAKILSVIWFPLTFLFGTLINGLAKRIFQIRSKNFILFLK 65 DR 3 NSTSTQPPDESCSNQNLITQQIPVLYCNUFAGILLNGSMWFFPVSSESSPFIYLN 62

Qy 66 TVISDILMLTFPKFLSDAKLGTGPLRFLFCVQTVSIFYFTMVISFLGLITIDRYQ 125 IVAIDPVMSIPTPKFLGQNLAKILSVIWFPLTFLFGTLINGLAKRIFQIRSKNFILFLK 63

Qy 67 TTRPEKTSNPKNLAKILSVIWFPLTFLFGTLINGLAKRIFQIRSKNFILFLK 65 DR 126 TTRPEKTSNPKNLAKILSVIWFPLTFLFGTLINGLAKRIFQIRSKNFILFLK 125 TTRPEKTSNPKNLAKILSVIWFPLTFLFGTLINGLAKRIFQIRSKNFILFLK 125

Qy 68 IVKPLWTSFQSVESKSKVSVVNLMLAVPNITLINSQSRREVTKQKCIELKSEGRK 182 DR 123 IVKPLWTSFQSVESKSKVSVVNLMLAVPNITLINSQSRREVTKQKCIELKSEGRK 182 IVKPLWTSFQSVESKSKVSVVNLMLAVPNITLINSQSRREVTKQKCIELKSEGRK 182

Qy 186 WHEINIVICIVIWFNLIVIVCUTLILKEIWSYVTRFGVGVPRKVNVTIIVF 245 DR 183 WHKASNYIVIWFNLIVIVCUTLILKEIWSYVTRFGVGVPRKVNVTIIVF 242 WHKASNYIVIWFNLIVIVCUTLILKEIWSYVTRFGVGVPRKVNVTIIVF 242

Qy 246 FICCPVPHPARIPYPLTSQPRDVFDTAENTFLVKESTWLTSLNACLDPFYFLCKSF 3.05 DR 243 FVCFVPHPARIPYPLTSQPRDVFDTAENTFLVKESTWLTSLNACLDPFYFLCKSF 3.05 FVCFVPHPARIPYPLTSQPRDVFDTAENTFLVKESTWLTSLNACLDPFYFLCKSF 3.02

RESULT 10

Q96JZ8 PRELIMINARY; PRT; 358 AA.

AC Q96JZ8; ID Q96JZ8; DR 01-DEC-2001 (TREMBLrel. 19, Created) 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE Hypothetical protein FL14878.

OS Homo sapiens (Human); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RC Placenta; RA Isobe T.; Ota T.; Hayashi K.; Sugiyama T.; Otsubo T.; Suzuki Y., Nishikawa T.; Nagai K.; Sugano S.; Shiratori A.; Sudo H.; Takahashi M.; Hosoi T.; Kaku Y.; Kodaira H.; Kondo H.; Sugawara M., Murakami K.; Ono Y.; Takiguchi S., Watanabe S.; Kimura K.; Yamamoto J.; Wakamatsu A.; Nakamura Y.; Saito K.; Ninomiya K.; Iwayanagi T., RT "NEDO human cDNA sequencing project"; RT Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

RL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL; AK027784; BAA55366.1; DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Genew; HGNC:4538; GPR87; Pfam; PF00001; 7tm_1..1; DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G PROTEIN RECEP_F1..1; DR PROSITE; PS50262; G PROTEIN RECEP_F1..2; DR Hypothetical protein; G-protein coupled receptor; Receptor; KW Transmembrane.

SEQUENCE . 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;

Query Match Score 39.3%; DB 4; Length 358; Best Local Similarity 42.6%; Pred. No. 1.2e-51; Matches 140; Conservative 67; Mismatches 113; Indels 9; Gaps 5;

Qy 6 NLTSARG-NTSLCTRDRYKITQVLFLPPLLTTVLFYVASTLNLGLAWIFFIRNKTSPIFYLK 64 DR 25 NRSDGPGNVTL--HNEDDTIVLPVXLIIFVYASLNLGLAWIFFIRNKTSPIFYLK 81

Qy 65 NTVISDLMILTFPKFLSDAKLGTGPLRFLFCVQTVSIFYFTMVISFLGLITIDRYQ 124 DR 66 NTVISDLMILTFPKFLSDAKLGTGPLRFLFCVQTVSIFYFTMVISFLGLITIDRYQ 124

Qy 67 NIVADLWMLTFPFRIVEDAGFPWYFKFILCRYSTVLYAMNTSIVLGLISIDRYL 141 DR 82 NIVADLWMLTFPFRIVEDAGFPWYFKFILCRYSTVLYAMNTSIVLGLISIDRYL 141

Qy 125 KTTRPEKTSNPKNLAKILSVIWFPLTFLFGTLINGLAKRIFQIRSKNFILFLKSERGL 184 DR 142 KVVKPGDGSQMYNTFTKYLISVCWVWMAVLSLENITNGQPTEDNHDCSKLSPLV 201

Qy 185 VWEHVNIVQCVIWINFLIVIVCYTLLKELYRSTYVTRGCVKVPRK-KVNVKVFILIA 243 DR 202 KMHTAVTYVNSCLPAVFLIGKXIA-SRYTHS-S-SRFQFISQSSRKRKHNSIRVVA 259

Qy 244 VFPIFVPHPARIPYPLTSQPRDVFDTAENTFLVKESTWLTSLNACLDPFYFLCK 303 DR 260 VFPIFVPHPARIPYPLTSQPRDVFDTAENTFLVKESTWLTSLNACLDPFYFLCK 319

Qy 304 SFRNSTL--SMLKCPNSAALSQDNRKE 330 DR 320 SFSRRLFKSNTRPSSESRSLSQSVRSE 348

RESULT 11

Q9BYZ1 PRELIMINARY; PRT; 358 AA.

AC Q9BYZ1; ID Q9BYZ1; DR 01-JUN-2001 (TREMBLrel. 17, Created) 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Orphan G protein-coupled receptor 87.

GN GPR87 OR GPR95.

OS Homo sapiens (Human); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=2117292; PubMed=11273702;

RX Wittenberger T.; Schaller H.C.; Hellebrand S.; DE "An expressed sequence tag (est) data mining strategy succeeding in

the discovery of new G-protein coupled receptors.";
J. Mol. Biol. 307:799-813(2001).
[2]
SEQUENCE FROM N.A.
MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., RA
Lewis T., Evans J.R., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled genes."
Gene 275:83-91(2001).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN CCC
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COU EMBL; AF237763; AA01858 1; -
DR EMBL; AF411114; AA026485 1; -
DR InterPro; IPR00276; GPCR_Rhodopsin.
Pfam; PF000001; 7tm 1; 1.
DR PRINTS; PS00237; GPCRRODOPSIN.
DR PROSITE; PS00232; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 358 AA; 41435 MW; DDF157295BESD10F CRC6 SQ
Query Match Score 694.5; DB 4; Le
Best Local Similarity 42.2%; Pred. No. 3.3e-51;
Matches 139; Conservative 68; Mismatches 113; In
Qy 6 NLTSARG-NTSLCTRDYKITQVLFPLPYTVLFPGVLITNGLM
Db 25 NRSGDGKNTL--HNEFDITVPLVLYLIFAVSTLNLGV
Qy 65 NTVISDMLMTPFPKLLSDAKGTGGLRTFVQVTSVIFTT
Db 82 NIIVAVLIMLWTFPFRVHDAGFPWYFKFLCRYSVLFAN
Qy 125 KTRRPFTNSPNKNLGAKILSYYTWAFMFLISLPNMILTNRQP
Db 142 KVKEPGDSRMTSITTFKVLSCVWVIMAVISLPLNITLINGDP
Qy 185 VWEHTIINYCQVIFWINFLIVCYCTLTKELYRSVYTRGVC
Db 202 KWHTAVTYVNSSLFVAVVILIGCYTAISRYIHKH--SRQFIS
Qy 244 VFFTCVVFPEHRARIPIYTLQSQRDVEDCTAENTLYKESTIWU
Db 260 VFFTCFLPYHICRIPPFTHSHLRLDDEAQKILYYCRBTILFV
Qy 304 SFRNSLI-SMILCPNSATSLSQDNRKKE 330
Db 320 SFSSRRFKKSNTTRSSSIRSUQSVRSE 348
RESULT 12
Q8CY47 PRELIMINARY; PRT; 358 AA.
ID Q8CY47; AC Q8CY47;
DT 01-MAR-2003 (P-TRMBLrel: 23, Created)
DT 01-MAR-2003 (TRMBLrel: 23, Last sequence update)
DT 01-MAR-2003 (TRMBLrel: 23, Last annotation update)
DE G-protein-coupled receptor 87.
OS Mus musculus (Mouse).
OC Metazoa; Chordata; Craniata; vertebrata;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID:10090;
RN [1]
RF SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus.
RC MEDLINE=22354683; PubMed=12466851;
RA The RIKEN Genome Exploration Research Group Phase I Consortium.
RA "Analysis of the mouse transcriptome based on function."
PT 60,770 full-length cDNAs."
RT Nature 420:563-573 (2002).
RT DR EMBL; AK080394; BAC37905.1; -

SQ	SEQUENCE	358 AA;	4141 MW;	6D58E9BCB3BEA9	CRC64;
	Query Match	38 - 6%;	Score 687;	DB 11;	Length 358;
	Best Local Similarity	41.0% ;	Pred. No. 1.4e-50;		
	Matches 141;	Conservative 63;	Mismatches 118;	Indels 22;	Gaps 5;
OY	7 LITSAGN-----TSLCPRD-----YKIQVLFPLLYTLFEGVLITGLNLAMRI 49				
Db	7 LTKLPENELYSQASHTANSTSEGHGNSTLNKEFTDLPLVLYLIVFVASTNLGIAWVI 66				
OY	50 PFGIERSKSNFTFLKNTVNSPMLLTFPKKILSDAKLGTPRLRPFVCQVTISVIFYFTMY 109				
Db	67 PPHIRNIKTSPTSFYLNINVVADLIMTFPPVIRVDRAGFGPKYEFELCRYISVLFYANM 126				
OY	110 ISISIFGLITIDRYORTTRPFKTSNPKNLNGAKILSVSIVIAFMFLILLSPNNTLNROPRD 169				
Db	127 TSIVFGLISSTDYLXVKPFGDSRMYSITFTKVLSCVWMAILSLLPNLITNGOPTK 186				
OY	170 KVKKCCSFLLSEFGLYWHETINYICQVIVFLNFLIVTCVCLTKEYLRSYTRTRGKV 229				
Db	187 ENIIDMMLKLSPLGKHMAYTVOSCLFLAVVLIGCCTAISRYHKS--SRQFSQS 244				
OY	230 PRK-KVNKVKEPIIIIAVFVICFPYPFHARIPYTLSQTRDVFDCTAENTLFYKTESTLWLT 288				
Db	245 SRKRKEHNQSIIVVVAFTCFPLPYHCRIPPTFSNIDRLDESAHKLLYYCKEMTILPLSA 304				
OY	289 LNACLDPIYFLCKSFRNSLI--SMLKCPNSATSLSQDNRKKE 330				
Db	305 CNVCLDPPIYPMCKSFSRRLFKKSNIRTSRSIRSLSQVRSE 348				
RESULT 13					
OY	Q99MT7 PRELIMINARY; PRT; 359 AA.				
ID	Q99MT7;				
AC	Q99MT7;				
DT	01-JUN-2001 (T-EMBLRelease 17; Last sequence update)				
DT	01-JUN-2003 (T-EMBLRelease 17; Last annotation update)				
DE	G-protein coupled receptor GPR87.				
CN	GPR87.				
OS	Mus musculus (Mouse)				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Murinae; Mus; NCBI_Taxid=10050;				
RN	[1] —				
RP	SEQUENCE FROM N.A. MEDLINE=21172992; PubMed=11273702;				
RX	RA Wittenberger T., Schaller H.C., Heilebrand S.; Created				
RA	"An expressed sequence tag (est) data mining strategy succeeding in the discovery of new g-protein coupled receptors.";				
RA	J. Mol. Biol. 307:799-813 (2001).				
RL	CC -; SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).				
CC	-; SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL; AF295366; AAK01866.1; -;				
DR	MGI; MGI:1934113; Gpr87.				
DR	InterPro: IPR000276; GPCR_RhoGDP.				
DR	Pfam; PF00001; Tcm_1; 1.				
DR	PRINTS; PR00237; GPCR_RHOGDP.				
DR	PROSITE; PS00231; G-PROTEIN RECEP_F1_1; 1.				
DR	PROSITE; PS50265; G-PROTEIN RECEP_F1_2; 1.				
RW	G-protein coupled receptor; Receptor; Transmembrane.				
SQ	SEQUENCE 359 AA; 41462 MW; 2EB313C2/73EFCD84;				
RESULT 14					
OY	38.6%; Score 685.5; DB 11; Length 359;				
Best Local Similarity	41.7%; Pred. No. 1.9e-50;				
Matches 136;	Mismatches 65; Indels 5; Gaps 3;				
OY	8 TSAPGNTSLCPRDYKTTQVLFPLLYTLFVGLITGLNLAMRFFQIQRSKSNFTIPLRNTY 67				
Db	26 STSEGHGNSTLNKEFTDLPLVLYIVFASILLGSLAVWFHFKNTSFIFLYRNIV 85				
OY	68 ISDLMLITFPKILSDAKLGTPRLRPFVCQVTISVIFYFTMYTISIPIGLLTDYRDTT 127				

RESULT 14

Q9BXC2 PRELIMINARY; PRT; 228 AA.

DB 86 VADLIMLTLEPFPRIVRDAGFGPWNFFEPFLCARYTSVLYANMYSIVPLGLISDVRKVV 145

QY 128 RPFKTSNPQLGAKLSSVIVAFMFLSLSPNMLTNRQPRDKVCKCSFLIKSERGLWNH 187

DB 146 KPFEDSRMSITFTKVLSCVWVMAISLSPNLTINGQPTKENIDCMKUSPLQAKWH 205

QY 188 EIVNYICQVIFWNLFLIVCYLTKEVYRTRGVKPRK-KVNFKVFLIIAVFF 246

DB 206 MATTYVDSCFLAVLIGCTAISRYHKS--SROFISQESRKHNOSIRVVAVFF 263

QY 247 ICFVPPFHARIPTLQLSQTRDVFCTAENTLFYKESTIWLTSNACLDPEFTFLCKSFR 306

DB 264 TCFPYHCKRIFTFSNDLRLBSAHKILYCKEMTLFLSACNVCLDPIYFPMCKSFS 323

QY 307 NSLI--SMLKCPNSATSLSQDNRKKE 330

DB 324 RLFKKSNIIRTSESISSLQSTRSE 349

RESULT 14

Q9BXC3 PRELIMINARY; PRT; 228 AA.

DB 01-JUN-2001 (TREMBLrel. 17, Created)

QY 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DB 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

EC 2.7.1.1.

RA Osada N.; Hida M.; Kubuda J.; Tanuma R.; Iseki K.; Hirai M.; Terao K.,

RA Suzuki Y.; Sugano S.; Hashimoto K.;

RA "Isolation of full-length cDNA clones from macaque brain cDNA libraries.", (MAR-2001) to the EMBL/Genbank/DDBJ databases.

DR ENBM: AB056816; BAB31942.1; -

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00037; GPROTEIN_RECGBP_F1_1; -

DR PRINTS: PS00237; G PROTEIN RECGBP_F1_2; -

DR PROSITE: PS50262; G-protein coupled receptor; -

DR SWISSPROT: MW; 1E7D98EE; 071756 CRC64;

SQ SEQUENCE FROM N.A.

RC TISSUE=Brain;

RC TISSUE=lung;

RC TISSUE=heart;

RC TISSUE=heart;

RA Strausberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

RL Submitted (JUN-2001) to the INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1. SUBCELLULAR LOCATION: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -1. SIMILARITY: AAU29069.1; -

DR EMBL; A2345556; AAU29069.1; -

DR BCO09540; AAU0940.1; -

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7em_1; 1

DR PRINTS; PS00237; G PROTEIN RECGBP_F1_1; -

DR PROSITE: PS50262; G-protein coupled receptor; -

DR SWISSPROT: MW; 31443; NM; 1E7D98EE; 071756 CRC64;

Query Match Score 553 5 DB 4 Length 269;

Best Local Similarity 42.5%; Pred. No. 2.4e-9;

Matches 111; Conservative 50; Mismatches 95; Indels 5; Gaps 3;

QY 73 MILTFPPFKLSDAKLGCGPLRIFCVQTVSIVFPTWNTISIPLGLLTDYKTKTPPKT 132

DB 1 MTLTFPPPRVHDAEGPMPYFKEFLCRATSVLFYANMMTSIVLGJSIDRTLKVKEFGD 60

QY 133 SNPNLIGAKLSSVIVAFMFLSLSPNMLTNRQPRDKVCKCSFLIKSERGLWNHVN 192

DB 61 SRVYSITFTPKVLSVWVMAISLSPNLTINGQPTENIDCSCKLSPGKHTAVY 120

QY 193 ICQVTFWNLFLIVCYLTKEVYRTRGVKPRK-KVNFKVFLIIAVFFFCVP 251

DB 121 VNSLFLFVAVLVIIGYIAISHNHS-SRFOISOSRZKHNQS-IVRVAVFFTCFLP 178

QY 252 FHPARIPPTLSQTRDVTCTAENTLFYKESTIWLTSNACLDPEFTFLCKSFRSLI 310

DB 179 YHLCRIPPTFSDRLLDSAQKILYCKETLFLSACNVCLDPIYFPMCRPSRFLK 238

QY 311 -SMUKCPNSATSLSQDNRKKE 330

DB 239 KSNTTRBESIRLQSYRSSE 259

Search completed: February 4, 2004 14:30:26

Job time : 42 secs

RESULT 15

Q9BXC2 PRELIMINARY; PRT; 269 AA.

DB 121 RONNCLERKSFVVAEVFVCAFPHTRVPTYSQNNKTDCLRNQNLTAKETFLA 180

QY 288 SINAACLDPEFTFLICKSFRNSLISMKCPNSATSLSDQRKKEQD 332

DB 181 ANTMCDPAPYIPICKETKPCMRGRKTIS--SODNOSSQTD 223

Copyright GenCore version 5.1.6
 (c) 1993 - 2004 Compugen Ltd.
 I protein - protein search, using sw model
 run on: February 4, 2004, 14:27:22 ; Search time 20 Seconds
 (without alignments)
 1644.484 Million cell updates/sec
 title: US-09-780-576-2
 wcrfct score: 1778
 sequence: 1 MQAVDNLTSAPGNTSLCPRD. SQDNRKKEQDGDPNEETPM 342
 scoring table: BLOSUM62

SEARCHED: INDEXED: SERIALIZED: FILED:
283308 96168682 7/21/96
SEARCHED INDEXED SERIALIZED FILED
ALIGNMENTS

number of hits each visit chosen parameters: 28220

卷之三

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

maximum matrix first 45

Phase I BIB 761

1: pirl:*

3: PIR3:*

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	394	22.2	342	2 A40191	platelet-activatin
2	392.5	22.1	342	2 S13638	platelet-activatin
3	379.5	21.3	361	2 B45680	G protein-coupled
4	366	20.6	341	2 S63666	platelet-activatin
5	362	20.4	341	2 S43252	platelet-activatin
6	357.5	20.1	308	2 I50241	G protein-coupled
7	339	19.1	359	2 S15403	angiotensin II rec
8	338	19.0	344	2 T09508	intron 17 purinerg
9	329	18.5	359	2 S139418	angiotensin II rec
10	326	18.3	359	2 S44425	angiotensin II rec
11	325.5	18.3	399	2 I48705	proteinase activat
12	325	18.3	359	2 A48857	angiotensin II rec
13	321	18.1	359	2 JC1104	angiotensin II rec
14	321	18.1	370	2 JC5549	heptahelical P275-
15	319	17.9	359	2 A42656	angiotensin II rec
16	319	17.9	359	2 JC2134	angiotensin II rec
17	318	17.9	359	2 JC1194	angiotensin II rec
18	318	17.9	359	2 JH0621	angiotensin II rec
19	317.5	17.9	365	2 S68208	G protein-coupled
20	317.5	17.9	398	2 I56517	mu opioid receptor
21	314.5	17.7	398	2 I56504	mu opioid receptor
22	314	17.7	359	2 J01516	angiotensin II rec
23	313.5	17.6	380	2 I38435	angiotensin recept
24	310.5	17.5	362	2 JN0694	angiotensin II rec
25	309	17.4	392	2 S65693	opioid receptor mu
26	309	17.4	400	2 I56553	mu opiate receptor
27	306	17.2	397	2 S66518	proteinase-activat
28	304.5	17.2	398	2 A57510	mu opioid receptor
29	299	16.8	380	2 TC2434	kappa opioid receptor

RESULT 1	A0191	platelet- C;Species- C;Accessi- P;Kunz, D J. Biol. A;Referen- A;Accessi- A;Molecul- A;Residue- A;Cross-r- R;Ife, R.D Biochem. A;Title: A;Title: A;Accessi- A;Molecul- A;Residue- A;Cross-r- A;Accessi- A;Status: A;Accessi- A;Molecul- A;Residue- A;Cross-r- R;Sugimoto Biochem. A;Title: A;Title: A;Accessi- A;Molecul- A;Residue- A;Cross-r- R;Seyfrie Genomics; A;Title: A;Referenc- A;Accessi- A;Molecul- A;Residue- A;Experiment: A;Note: t R;Chase, J Am. J. Be-
----------	-------	--

ALIGMENTES

RESULT 1	A0191 platelet- C;Species- C;Accessi- P;Kunz, D J. Biol. A;Referen- A;Accessi- A;Molecul- A;Residue- A;Cross-r- R;Ife, R.D Biochem. A;Title: A;Title: A;Accessi- A;Molecul- A;Residue- A;Cross-r- A;Accessi- A;Status: A;Accessi- A;Molecul- A;Residue- A;Cross-r- R;Sugimoto Biochem. A;Title: A;Title: A;Accessi- A;Molecul- A;Residue- A;Cross-r- R;Seyfrie Genomics; A;Title: A;Referenc- A;Accessi- A;Molecul- A;Residue- A;Experiment: A;Note: t R;Seyfrie Genomics; A;Title: A;Referenc- A;Accessi- A;Molecul- A;Residue- A;Experiment: A;Note: s R;Chase, J Am. J. Be-
----------	--

			G protein-coupled		
3.0	298.5	16.8	365	2	568679
3.1	298	16.8	480	2	48827
3.2	297.5	16.7	359	2	151372
3.3	297.5	16.7	360	2	A53611
3.4	297	16.7	380	2	A55259
3.5	296.5	16.7	420	2	151667
3.6	296	16.6	380	2	S316143
3.7	295	16.6	380	2	JC2338
3.8	292.5	16.5	362	2	S33733
3.9	291.5	16.4	373	2	A37556
4.0	290.5	16.3	352	2	A45747
4.1	284.5	16.0	333	2	I38974
4.2	282	15.9	352	2	G00048
4.3	282	15.9	352	2	A43113
4.4	281.5	15.9	355	2	SQ2131
4.5	281.5	15.8	353	2	SQ8787

ALIGMENTS

NULL 1
residues: 1-315; type: mRNA
holoclelue type: mRNA
residues: 1-342 <KIN>
cross-references: GB:MB0436; NID:9456674; PIDN:AAA60002.1; PID:g456294
experimental source: R.D.; Prosnitz, E.R.; Zou, A.; Cochran, C.G.
Chemical Biophys. Res. Commun. 180, 105-111, 1991.
Title: Characterization of a human cDNA that encodes a functional receptor for platelet-activating factor receptor number: JH0479; MUID:92028922; PMID:1656963
accession: A40191; MUID:92250505; PMID:1374385
holoclelue type: mRNA
residues: 1-342 <YER>
cross-references: GB:D0433; NID:9189337; PIDN:AAA60001.1; PID:g189338
experimental source: granulocyte, cell line HL-60 all
Makukamura, M.; Honda, Z.; Izumi, T.; Sakakata, C.; Maroh, H.; Minami, M.; Bito, H.; S
Biol. Chem. 266, 20400-20405, 1991.
Title: Molecular cloning and expression of platelet-activating factor receptor from
reference number: A41079; MUID:920241873; PMID:1657923
accession: A41079
status: not compared with conceptual translation
holoclelue type: mRNA
residues: 1-342 <NAK>
cross-references: GB:D10202; GB:D90433; NID:9219975; PIDN:AAA01050.1; PID:g219976
experimental source: Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.
Chem. Biophys. Res. Commun. 189, 617-624, 1992.
Title: Molecular cloning and characterization of the platelet-activating factor receptor rece
reference number: JC1359; MUID:93112021; PMID:1281995
holoclelue type: mRNA
residues: 1-315; 'N', 311-342 <SUG>
experimental source: heart
note: the authors translated the codon AAT for residue 316 as Lys
Seiffert, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
Biomolecules 13, 832-834, 1992.
Title: The human platelet-activating factor receptor gene (PTAFR) contains no intron
reference number: A42831; MUID:92347896; PMID:1322356
holoclelue type: DNA
residues: 1-226; 'TG', 222-342 <SEY>
cross-references: GB:MB8177; NID:9190697; PIDN:AAA60214.1; PID:9190698
experimental source: sequence extracted from NCBI backbone (NCBIN:109813, NCBI:109814)
Seiffert, C.E.; Halonen, M.; Regan, J.W.
J. Biomol. Cell Mol. Biol. 8, 240-244, 1993.

A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for an A;Reference number: MUID:151923; PMID:3319235; FMID:8383307	A;Accession number: 151923	A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA	A;Residues: 1-342	A;Cross-references: GB:556396; NID:9298580; PIDN:AAB25755..1; PID:9298581
C;Genetics:		
A;Gene: GDB:PNAAFR		
A;Cross-references: GDB:129806; OMIM:173393		
A;Map position: 1p3-1p3.3		
C;Superfamily: ATP receptor P2u		
C;Keywords: G protein-coupled receptor; transmembrane protein		
F:17-38 /Domain: transmembrane #status predicted <TRI>		
F:54-75 /Domain: transmembrane #status predicted <TRI>		
F:92-113 /Domain: transmembrane #status predicted <TRI>		
F:114-155 /Domain: transmembrane #status predicted <TRI>		
F:184-205 /Domain: transmembrane #status predicted <TRI>		
F:233-253 /Domain: transmembrane #status predicted <TRI>		
F:277-297 /Domain: transmembrane #status predicted <TRI>		
Query Match 22.2%; Score 394; DB 2; Length 342;		
Best Local Similarity 32.6%; Pred No. 1.5e-26;		
Matches 107; Conservative 61; Mismatches 134;		
Indels 26; Gaps 10;		
Qy 11 PGNTSLCTRDYKITYWLFPLLYTVPFGLITNGLAMRIFFOIR--SKSNPFI-IFLKNTY 67		
Db 3 PHDSSMDSEPYT--LFPIVYSSIFVLGIVANGIVLNFAIRLYPKCKEENIKIFMWNL 60		
Qy 68 ISDLMILTPPFKILSDAKIGTGPRLTFVQCYTSVLYFTYTMISISFLGLITDRYQTT 127		
Db 61 MADMLFLITPLWIVYYQNQGNWILPKFLCNVAGLUFFINTYCVAFGVITYNRFQAVT 120		
Qy 128 RPFKTSNPKNLJGAKILSIVVITW---AFMFLLSLPNMLTNRQPRDK--NVRKCSTJK 179		
Db 121 RPIKTAQANTERKGKISLISLIVIWAIVGAASYFLIDS--TNTYPSAGSGNYTRC-FEH 176		
Qy 180 SEFGFLYWHETINYTCQVFWINFLIVIVCYTLTKELYRSYVTRGKVPRKVNVYF 239		
Db 177 YEKGSPVLIHIFIYFSFLIVLFLFCMVLVITLLMOPQQORNARTVKRALWM-VC 235		
Qy 240 IIIAVFPCFVPPHFARIPIYPLSOTRDFVCTAENTLFYKESTIWLTNSNACLDPPFTYP 299		
Db 236 TVLAVFPCFVHHVQLPWTLAEI-GFDQDSKPHQAINDAHQVTLCLLSTNCVDPVYTC 294		
Qy 300 FLCKSPRN----SLISMILKCPNSAT 320		
Db 295 FLTKKPFKHLTEKFYSMRSSSRCSRATT 322		
RESULT 2		
S13638 platelet-activating factor receptor - guinea pig		
C;Species: Cavia porcellus (guinea pig)		
C;Accession: S13638		
R;Honda, Z.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To		
Nature 349, 342-346, 1991		
A;Title: Cloning by functional expression of platelet-activating factor receptor from guinea pig		
A;Reference number: S13638; MUID:91101726; PMID:1846231		
A;Status: preliminary		
A;Molecule type: tRNA		
A;Residues: 1-342 <HN>		
Query Match 22.1%; Score 392.5; DB 2; Length 342;		
Best Local Similarity 30.7%; Pred. No. 2.1e-26;		
Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;		
C;Superfamily: ATP receptor P2u		
20 DYKITQVLFPLLYTVPFVGGLITNGLAMRIFQI-RSKSNPFI-IFLKNTVISDILMLT 76		

```

RESULT 4
S63666
Platelet activating factor receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S63666
R/Ishii, S.; Matusuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Shimizu, T.
Biochem. J. 314, 671-678, 1995
A;Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization
A;Reference number: S63666; MUID:96239129; PMID:9570084
A;Accession: S63666
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-341 <TSH>
A;Cross-references: 1-341; EMBL:DS0872; NID:gi1256924; PID:BA09468.1; PID:gi1256925
C;Superfamily: ATP receptor P2u

Query Match Score 20.6%; DB 2; Length 341;
Best Local Similarity 29.9%; Pred. No. 4e-24;
Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;
Qy 20 D Y K I T O V L F P U Y T V I F F V G I T I G A M R I F F Q I - R S K E N F I - I F L K I N T V I S D I L M I L T 76
Db 10 D S E F R Y T L F P I V S V I F L G V A N G Y L W T P A N L Y P S K C L N B K F M V N L T M A D I L F I T 69
Qy 77 F P F K I L S D A K L G T G P L R T F C Q V T S V I F Y F T M Y S I S F L G L I T I D R Y Q K T R P K T S N P K 136
Db 70 I P L W I Y Y P N G D W I L F N L E N V A G L F F I N T Y C S A F L G I T I N T R Y Q A Y P K T Q A T 129
Qy 137 N I L G A X I L S V Y V I W A F M - - - F L I S P N M I L T N R Q P R D K N V K C S F L K S R F G - - - L Y W H E 188
Db 130 T R K R G I S L S L I W V S I T A S Y F L A D S T I N V P N K D G S G N I T C P H Y E P Y S V P I L V V H 189
Qy 189 I V N Y I C O V I F W I N F I L I V I V C Y T I L T K E Y L P S Y V P T R G / G K V P R K V N V K V P I I V A F F I 247
Db 190 F I A F C F P L V F F U F I Y C N L V I H T L I T Q P M R Q Q - - R E A G V - - - K E R A L N V V C T V I A V F I I 243
Qy 248 C F V P F F H A R I P Y T L S Q T R D V F D C T A N T L F V K E S T I W L I S L N A C D P F Y F F L K S F R N 307
Db 244 C F V P H P V V Q U P W I P W I L A E I G - - Y O T N F H Q A I N D A H O T T U C L I J S T C N C V I D P V I Y C P T K K F R K 301
Qy 308 - - - - - S L I S M L K C P N S A T S 321
Db 302 H I S E K F Y S M R S S R K C - S R A T S 321

RESULT 5
S43252
platelet-activating factor receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C;Accession: S43252
R/Bito, H.; Honda, Z.; Nakamura, M.; Shimizu, T.
Bur. J. Biochem. 221, 211-218, 1994
A;Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-receptor
A;Reference number: S43252; MUID:9422063; PMID:8168510
A;Accession: S43252
A;Molecule type: mRNA
A;Residues: 1-341 <BT>
A;Cross-references: 1-341; GB:U04740; NID:gi9470384; PID:AAA18422.1; PID:gi470385
C;Superfamily: ATP receptor P2u

Query Match Score 20.4%; DB 2; Length 341;
Best Local Similarity 28.9%; Pred. No. 8.e-24;
Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;
Qy 20 D Y K I T O V L F P U Y T V I F F V G I T I G A M R I F F Q I R S K S N F I I F L K I N T V I S D I L M I L T 76
Db 10 D S E F R Y T L F P I V S V I F L G V A N G Y L W T P A N L Y P S K C L N B K F M V N L T M A D I L F I T 69

```

QY	77	FPKILSDAKLGTGPFLRPFVQCVTSVIFVFFTMVISISIGLITIDRYQKTRFXTSPK	136
Db	70	LPLWIVVLSNEGDWIKHKLCLNAGCFLPINTYCSVALGIVTYNRYQAVAYDIAQAT	129
QY	137	NLLGAKILSVVIAWM-----FLISLSPNLLINRQPRDRGNVKCC-----S	176
Db	130	TKRGITLISVVISSIAATASYFLATDSNNVVKDKGGSGNITRCFEHTEPVSYPLVYTHI	189
QY	177	FLKSFPGLYWHEITVNYICCVIFWIFNLFIVCYTLLTBEVLYSYVRTGVGVPRKKYNN	236
Db	190	FITSCPFLVFF-----LIFYCNMVII---HTLLTRP----VRQQRKPEVKRRAWM	233
QY	237	KVFIILAVFICFVYTFPHFRIPIPTFSQRDVFDTAAENTLFTYKESTIWLTSNSACLDPF	296
Db	234	-VCTVTLAVFVICFVPHAVYQLPWTIAEG--YQTNFHQAINDAHQITCLSLNCVLDPV	290
QY	297	TYPFLCKSPRN-----SLISMHKCPNSATS	321
Db	291	IYCFLTTRKPRKHLSERFKTSMRSRKC-SRATS	321
RESULT 6			
	150241	G protein-coupled receptor 6H1 - chicken	
C;Species:	Gallus Gallus (chicken)		
C;Accession:	13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000		
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.	J. Immunol. 151, 628-636, 1993		
A;Title:	Identification of a G protein coupled receptor induced in activated T cells		
A;Reference number:	150241; MUID:93329058; PMID:8393036		
A;Accession:	150241		
A;Status:	Preliminary; translated from GB/EMBL/DBJ		
A;Molecule type:	mRNA		
A;Residues:	1-308 <WEB>		
A;Cross-references:	GB:L06109; NID:9304383; PIDN:AA06587.1; PID:G304384		
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.	Biochem. Biophys. Res. Commun. 219, 105-110, 1996		
A;Title:	Identification of 6H1 as a P2Y purinoreceptor: P2Y5.		
A;Reference number:	JCA618; MUID:96190677; PMID:8613790		
A;Accession:	JCA618		
A;Molecule type:	mRNA		
A;Residues:	1-308 <WEB>		
A;Cross-references:	GB:L06109; NID:9304383; PIDN:AA06587.1; PID:G304384		
A;Experimental source:	T-cells		
C;Comment:	This receptor plays a role in T-cell activation.		
A;Gene:	P2Y5		
C;Superfamily:	ATP receptor P2U		
C;Keywords:	G protein-coupled receptor; transmembrane protein		
F;15-40/Domain:	transmembrane #status predicted <TM1>		
F;51-74/Domain:	transmembrane #status predicted <TM2>		
F;89-109/Domain:	transmembrane #status predicted <TM3>		
F;113-153/Domain:	transmembrane #status predicted <TM4>		
F;177-201/Domain:	transmembrane #status predicted <TM5>		
F;227-248/Domain:	transmembrane #status predicted <TM6>		
F;269-292/Domain:	transmembrane #status predicted <TM7>		
Query Match	20.1%	Score 357.5; DB 2; Length 308;	
Best Local Similarity	29.5%;	Pred. No. 1_9e-23;	
Matches	87;	Mismatches 125; Indels 15; Gaps 8;	
QY	14	TSCLTRDYYKTQVFLGPFLRPFVGLTNGLAMRIP-FQIRKSNNFLFLQNTVTSIDL	72
Db	3	SSNCSTDPSRPTYVGCFSMVFTFLCISTDFRLATVHPRS	62
QY	73	MILTPPEKILSDAKLGTGPFLRPFVGLTNGLAMRIP-FQIRKSNNFLFLQNTVTSIDL	72
Db	63	FVFTLPLRFLYFYV-WRNPPGFVYFLCKISSTLEFTNMCSILFLTCISTDFRLATVHPRS	121
QY	133	SNPKNLGAKILSVVIAWMFLLSPNMLL-TNRQPRDKNVKCC--SPLKSEGLVWHE	188

Db 122 KTLRKRNARIVCVAVWITLAGSTPASFFQSTNTRQ-NNTERRQTCPENFPEETWKTYSR 180
 C;Cross-references: EMBL:AF000546; NID:92232068; PID:92232069
 C;Genetics:
 A;Map position: 13
 C;Superfamily: G-protein coupled receptor P2u
 C;Keywords: G protein-coupled receptor; transmembrane protein

Db 189 IVNICQVIFVYIINFLIVTVCYLITKELYSTYRTRGVKPVKRNVKVFTIAVEFIC 248
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C;Date: 19-Mar-1997
 Db 181 IVIFELIVGPFPLILNTCSTMVLTNLKPLTSR--NKLSKKVYLKOMIPHLVIFCFC 238
 C;Accession: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
 C;Date: 16-Jul-1999
 Qy 249 FVPPHEFARIPIYTLQSOTRDVFDC--TAENTLYVKESTIWLTSLNACLDPPFYFP 300
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C;Date: 19-Mar-1997
 Db 239 FVWNITLILYSLNRQTQMINCSVTAVRTMVKY--TLCIANSNCEDPTVYFP 290
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C;Date: 19-Mar-1997

RESULT 7

S15443 angiotensin II receptor type 1 - bovine
 C;Species: Bos primigenius indicus x Bos primigenius taurinus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C;Accession: S15443
 R:Sasaki, K.; Yamato, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
 Nature 351, 230-233, 1991.
 A;Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin II receptor type 1.
 A;Reference number: S15443; PMID:91253900; PMID:2041569
 A;Accession: S15443
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-359 <SAS>
 A;Cross-references: GB:X62294; NID:943; PIDN:CAA44182.1; PID:944
 C;Superfamily: vertebrate rhodopsin

Query Match 19.1%; Score 339; DB 2; Length 359;
 Best Local Similarity 27.9%; Pred. No. 9e-22;
 Matches 95; Conservative 62; Mismatches 143; Indels 40; Gaps 10;

Db 26 VLFPOLITYVLFVGLITNLGL-AMRIFFQIRSKNSNFIILKNTVTSIDLMLIDPPFKLSD 34
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Db 29 MIPIYLISLTFVGGIFGNSLVIVTVYFNMKLKTYASVFLNLALADICFLCLPLWAVYT 88
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Qy 85 ARLGTPGLTRFVQVTTVYFVNTMISIISLGLITDIDRYQKTRPFTKSNPKNLGGAKIL 144
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Db 89 AMEYKMPFGNYLCKIASVSYFLNLVYASVFLNLCLSIDRLYVHMPMSRLRLTMLVAKY 148
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Qy 145 SVVIVAFMFLLSPNMLTN-RQPRDKNTVCKSF-----I-KSEFGLVWHEBIVNYTCQ 195
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Db 149 CIIIWLAGSLPTIIRNNVFFLENTNTVCAHYESONSTLPVGLLT-KNIGLPL-- 205
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Qy 196 VIFWMNFLITYVCYLITKELYSTYRTRGVKPVKRNVKVFTIAVEFICFVPPFHA 255
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Db 206 ----EPFLIITSYTIIWKLRKEIQK--NKRKDQFILKATIYVLFPPF-----FS 252
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Qy 256 RIPYTLQSOTRDVF-----DCTAENTLYVKESTIWLTSLNACLDPPFYFLICKSFRNS 308
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Db 253 WVPHQIETMVLQIGLDRCKTIEDVAMPITICLAYFNNLNPFLYFGKKEFRKY 312
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Qy 309 IJISMLK-CPNSATSLSQDNRK----REQDGGDPNEETP 341
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 Db 313 FLQLKXYPPIAKSHSNLSTMSTLSYRSPENGNSSTKRP 352
 C;Accession: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999

RESULT 8

T09508 intron 17 purergic receptor P2Y5 - human
 N;Alternate names: G-protein coupled receptor
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
 C;Accession: T09508
 R;Bom, S.K.; Trumpp, A.; Khatun, L.M.; Kong, W.; Payan, D.G.; Bennett, N.W.
 Submitted to the EMBL Data Library, April 1997
 A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene.
 A;Accession: T09508
 A;Status: preliminary; translated from GB/ENBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-344 <BOH>

Query Match
Best Local Similarity 18.3%; Score 326; DB 2; Length 359;
Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 8;
Query 26 VLFPLIYVTLFVGLITGL-AMRIIFRISKSNSNFIPLKNTVISDILMLTFPPKILSD 84
Db 29 VMIPFLYSTIIVFGNLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 85 AKLGTGPRTFCQTYCSTIIFTYTMYSISFLGHTIDRYQKTRPFTSNSNPKNLGAKIL 144
Db 89 AMEYRWPGNYLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 145 SVTYWAFMELLSLPNMILTN-RQPRDKNVKCSF-----LKSERGLYVHEIINYICQ 195
Db 149 CITWLLGLASLEPTIIRNVIFFLENITIVAHYEQSNSTLPIGLGLT-KNIGFL-- 205
Query 196 VIFWINFELIVIVCYTLIKELYSYVTRGVKVRPKVKVYKVEI-LIAVFFICYPFHF 254
Db 206 ---FPFLTSLTSLTLYKRAYEIQK---NKPRDDIFKIMAIVLVPLFVWPHQI 258
Query 255 ARIPYTLGOSTRDQFDCAENTLYKVESTLWTSLNACLDPIFYFLICKSPRNSLISMK 314
Db 259 FTFLDVQLQGITHDCKLADIVDTAMPMTICAYFNCLNPFLFYGFGLKFKYFLQLK 318
Query 315 -CPNSATSLSQDNRK 328
Db 319 YIPPKAKHESLSRK 333

Query Match
Best Local Similarity 18.3%; Score 325; DB 2; Length 359;
Matches 92; Conservative 55; Mismatches 146; Indels 22; Gaps 8;
Query 26 VLFPLIYVTLFVGLITGL-MRIFQRSNSNFIPLKNTVISDILMLTFPPKILSD 84
Db 29 VMIPFLYSTIIVFGNLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 85 AKLGTGPRTFCQTYCSTIIFTYTMYSISFLGHTIDRYQKTRPFTSNSNPKNLGAKIL 144
Db 89 AMEYRWPGNYLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 145 SVTYWAFMELLSLPNMILTN-RQPRDKNVKCSF-----LKSERGLYVHEIINYICQ 195
Db 149 CITWLLGLASLEPTIIRNVIFFLENITIVAHYEQSNSTLPIGLGLT-KNIGFL-- 205
Query 196 VIFWINFELIVIVCYTLIKELYSYVTRGVKVRPKVKVYKVEI-LIAVFFICYPFHF 254
Db 206 ---FPFLTSLTSLTLYKRAYEIQK---NKPRDDIFKIMAIVLVPLFVWPHQI 258
Query 255 ARIPYTLGOSTRDQFDCAENTLYKVESTLWTSLNACLDPIFYFLICKSPRNSLISMK 314
Db 259 FTFLDVQLQGITHDCKLADIVDTAMPMTICAYFNCLNPFLFYGFGLKFKYFLQLK 318
Query Match

RESULT 10
S44425 angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
PEBS Lett. 343: 146-150, 1994
A;Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
A;Reference number: S44425; MUID:94222188; PMID:8168620
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Cross-references: PIDN:AAB30674.1; PID:95446569
A;Experimental source: liver
C;Superfamily: vertebrate rhodopsin
A;Residues: I-359 <BUR>
A;Cross-references: PIDN:AAB30674.1; PID:95446569
C;Superfamily: vertebrate rhodopsin
Query Match
Best Local Similarity 29.2%; Score 326; DB 2; Length 359;
Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 8;
Query 26 VLFPLIYVTLFVGLITGL-AMRIIFRISKSNSNFIPLKNTVISDILMLTFPPKILSD 84
Db 29 VMIPFLYSTIIVFGNLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 85 AKLGTGPRTFCQTYCSTIIFTYTMYSISFLGHTIDRYQKTRPFTSNSNPKNLGAKIL 144
Db 89 AMEYRWPGNYLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 145 SVTYWAFMELLSLPNMILTN-RQPRDKNVKCSF-----LKSERGLYVHEIINYICQ 195
Db 149 CITWLLGLASLEPTIIRNVIFFLENITIVAHYEQSNSTLPIGLGLT-KNIGFL-- 205
Query 196 VIFWINFELIVIVCYTLIKELYSYVTRGVKVRPKVKVYKVEI-LIAVFFICYPFHF 254
Db 206 ---FPFLTSLTSLTLYKRAYEIQK---NKPRDDIFKIMAIVLVPLFVWPHQI 258
Query 255 ARIPYTLGOSTRDQFDCAENTLYKVESTLWTSLNACLDPIFYFLICKSPRNSLISMK 314
Db 259 FTFLDVQLQGITHDCKLADIVDTAMPMTICAYFNCLNPFLFYGFGLKFKYFLQLK 318
Query Match
Best Local Similarity 27.6%; Score 325; DB 2; Length 359;
Matches 92; Conservative 73; Mismatches 141; Indels 27; Gaps 12;
Query 22 KITOYLFLPYLTYFFVGLITGL-AMRIIFRISKSNSNFIPLKNTVISDILMLTFPPKILSD 80
Db 74 KLTTVFLPPIVIIIVFVIGPSNGMALWFLFRKGKPAVINMANLADLSIVNPLK 133
Query 81 ILSDAKLGTGPLRTFCQTYCSTIIFTYTMYSISFLGHTIDRYQKTRPFTSNSNPKNLG 140
Db 134 ISYHLRGNNWVYGAFLCKVLLGFLPYGNNSCSILEMTCLSVQYWVITNPM-GHPRKAN 191
Query 141 AKI-LSVVIWAEMFLSLPML-TNQPRDKNVKCSFELKSEPLGFLYVHEIINYICQ- 196
Db 192 IAVEVSLAWLFLVTPLYMKQTIIYPA-LNITTCVDPLEEVIV-GDNMFNFUSLA 249
Query 197 -IFWINFLIVIVCYTLIKELYSYVTRGVKVRPKVKVYKVEI-LIAVFFICYPFHF 254
Db 250 IGVLFLPMLTAASVYMLKTLSANDHSERK-RQAIRLILITVLYATYCFCFAASN 307
Query 255 AR-IPYTLGOSTRDQFDCAENTLYKVESTLWTSLNACLDPIFYFLICKSPRNSLISM 313
Db 308 LIVVHYEJLKTQ-----QSHTYALVVALCLSTLNSCIDPFVYFVSQDFRDHARNL 361
Query 314 KCPNSAT-----SLSQNRKEQDGDPNEET 340
Db 362 LCRSVRTVNRMQISLS-SNKFSRKSGSYSSST 393
Query Match
Best Local Similarity 18.3%; Score 326; DB 2; Length 359;
Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 8;
Query 26 VLFPLIYVTLFVGLITGL-AMRIIFRISKSNSNFIPLKNTVISDILMLTFPPKILSD 84
Db 29 VMIPFLYSTIIVFGNLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 85 AKLGTGPRTFCQTYCSTIIFTYTMYSISFLGHTIDRYQKTRPFTSNSNPKNLGAKIL 144
Db 89 AMEYRWPGNYLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 145 SVTYWAFMELLSLPNMILTN-RQPRDKNVKCSF-----LKSERGLYVHEIINYICQ 195
Db 149 CITWLLGLASLEPTIIRNVIFFLENITIVAHYEQSNSTLPIGLGLT-KNIGFL-- 205
Query 196 VIFWINFELIVIVCYTLIKELYSYVTRGVKVRPKVKVYKVEI-LIAVFFICYPFHF 254
Db 206 ---FPFLTSLTSLTLYKRAYEIQK---NKPRDDIFKIMAIVLVPLFVWPHQI 258
Query 255 ARIPYTLGOSTRDQFDCAENTLYKVESTLWTSLNACLDPIFYFLICKSPRNSLISMK 314
Db 259 FTFLDVQLQGITHDCKLADIVDTAMPMTICAYFNCLNPFLFYGFGLKFKYFLQLK 318
Query Match
Best Local Similarity 18.3%; Score 325; DB 2; Length 359;
Matches 92; Conservative 55; Mismatches 146; Indels 22; Gaps 8;
Query 26 VLFPLIYVTLFVGLITGL-MRIFQRSNSNFIPLKNTVISDILMLTFPPKILSD 84
Db 29 VMIPFLYSTIIVFGNLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 85 AKLGTGPRTFCQTYCSTIIFTYTMYSISFLGHTIDRYQKTRPFTSNSNPKNLGAKIL 144
Db 89 AMEYRWPGNYLCKIASVSNLIVYASVFLTCLSLIDRYVALVHPMKSPVRITMLMAKV 148
Query 145 SVTYWAFMELLSLPNMILTN-RQPRDKNVKCSF-----LKSERGLYVHEIINYICQ 195
Db 149 CITWLLGLASLEPTIIRNVIFFLENITIVAHYEQSNSTLPIGLGLT-KNIGFL-- 205
Query 196 VIFWINFELIVIVCYTLIKELYSYVTRGVKVRPKVKVYKVEI-LIAVFFICYPFHF 254
Db 206 ---FPFLTSLTSLTLYKRAYEIQK---NKPRDDIFKIMAIVLVPLFVWPHQI 258
Query 255 ARIPYTLGOSTRDQFDCAENTLYKVESTLWTSLNACLDPIFYFLICKSPRNSLISMK 314
Db 259 FTFLDVQLQGITHDCKLADIVDTAMPMTICAYFNCLNPFLFYGFGLKFKYFLQLK 318
Query Match
Best Local Similarity 18.3%; Score 325.5; DB 2; Length 359;

Db 319 YIPPAKAKSHSNLSTK 333

RESULT 13
 JCI104 angiotensin II receptor type 1 - human
 N;Alternate names: angiotensin II receptor 1A
 C;Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text_change 21-Jul-2000
 R;Maizy, C.A.; Hwang, C.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
 Biomed. Biophys. Res. Commun. 186, 277-284, 1992
 A;Title: Cloning, expression, and characterization of a gene encoding the human angiotensin II receptor. PMID:1378723
 A;Accession: JCI104
 A;Molecule type: DNA
 A;Residues: 1-359 <DNA>
 R;Furuta, H.; Guo, D.F.; Inagami, T.
 Biochem. Biophys. Res. Commun. 183, 8-13, 1992
 A;Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
 A;Reference number: JQ1402; MUID:52337608; PMID:1543512
 A;Accession: JQ1402
 A;Molecule type: DNA
 A;Residues: 1-159 <DNA>
 A;Cross-references: EMBL:211162; PID:928709; PID:g287010
 A;Experimental source: lymphocyte
 R;Bergsma, D.J.; Ellis, C.; Kumar, C./ Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.; G.
 Biochem. Biophys. Res. Commun. 183, 989-995, 1992
 A;Title: Cloning and characterization of a human angiotensin II type 1 receptor.
 A;Accession: JH0574
 A;Molecule type: mRNA
 A;Residues: 1-159 <BER>
 A;Experimental source: liver
 R;Takayama, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Haji, M.; Imagami, T.; F.
 Biochem. Biophys. Res. Commun. 183, 910-916, 1992
 A;Title: Molecular cloning, sequence analysis, and expression of a cDNA encoding human type
 A;Reference number: JH0267; MUID:92198490; PMID:1550596
 A;Accession: JH0267
 A;Molecule type: mRNA
 A;Residues: 1-159 <TAK>
 A;Experimental source: liver
 R;Currow, K.M.; Pascoe, L.; White, P.C.
 Mol. Endocrinol. 6, 1113-1118, 1992
 A;Title: Genetic analysis of the human type-1 angiotensin II receptor.
 A;Accession: A44014
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-159 <CUR>
 A;Cross-references: GB:MR3394; NID:9178680; PID:9178681
 A;Note: sequence extracted from NCBI backbone (NCBIN:111831, NCBIPI:111833)
 C;Genetics:
 A;Gene: GDB:AGTR1
 A;Cross-references: GDR:1132359; OMIM:106165
 A;Map Position: 3q21.3q25
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane
 P;30-5-/Domain: transmembrane #status predicted <TM1>
 P;65-80-/Domain: transmembrane #status predicted <TM2>
 P;103-124-/Domain: transmembrane #status predicted <TM3>
 P;145-167-/Domain: transmembrane #status predicted <TM4>
 P;194-216-/Domain: transmembrane #status predicted <TM5>
 P;241-264-/Domain: transmembrane #status predicted <TM6>
 P;281-305-/Domain: transmembrane #status predicted <TM7>
 P;4,176,188-/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14
 JCS549 heptahelical P2Y5-like receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
 C;Accession: JC5549
 R;Boeynaems, J.M.; Godart, M.; Communi, D.
 Biochim. Biophys. Res. Commun. 236, 106-112, 1997
 A;Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
 A;Reference number: JC5549; MUID:736605; PMID:922335
 A;Accession: JC5549
 A;Molecule type: DNA
 A;Residues: 1-370 <JAN>
 A;Cross-references: DDBJ:JA005419; NID:G2240034; PID:G2240034; PID:G2240035
 C;Superfamily: ATP receptor P2u

Query Match 15
 JCS549 Best Local Similarity 27.7%; Pred. No. 3-3e-20;
 Matches 87; Conservative 67; Mismatches 134; Indels 26; Gaps 9;

Query Match 16
 JCS549 7 ITSAPNTSLICRDYKITOVLIFPLIYTFVQVTSVITYFTMYSISLGLITDRLN 65
 A;Molecule type: DNA
 A;Accession: JC5549
 R;Lavsdil, F.; Veltman, R.H.P.G.D.L.C.K.; SGTAPLTNIGSMLELTCSVDRLFA 139
 A;Residues: 1-370 <JAN>
 A;Cross-references: DDBJ:JA005419; NID:G2240034; PID:G2240035
 C;Superfamily: ATP receptor P2u

Query Match 17
 JCS549 126 TTRPFTSNPKNLGAKILSVIAVAFMEYLSPAMMLTRQPRDKVKNKCSPLKSEFGI- 184
 A;Molecule type: DNA
 A;Accession: JC5549
 R;Lavsdil, F.; Veltman, R.H.P.G.D.L.C.K.; SGTAPLTNIGSMLELTCSVDRLFA 139
 A;Residues: 1-370 <JAN>
 A;Cross-references: DDBJ:JA005419; NID:G2240034; PID:G2240035
 C;Genetics:
 A;Gene: GDB:AGTR1
 A;Cross-references: GDR:1132359; OMIM:106165
 A;Map Position: 3q21.3q25
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane
 P;30-5-/Domain: transmembrane #status predicted <TM1>
 P;65-80-/Domain: transmembrane #status predicted <TM2>
 P;103-124-/Domain: transmembrane #status predicted <TM3>
 P;145-167-/Domain: transmembrane #status predicted <TM4>
 P;194-216-/Domain: transmembrane #status predicted <TM5>
 P;241-264-/Domain: transmembrane #status predicted <TM6>
 P;281-305-/Domain: transmembrane #status predicted <TM7>
 P;4,176,188-/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18
 JCS549 Best Local Similarity 28.7%; Pred. No. 3.2e-20;
 Matches 92; Conservative 56; Mismatches 139; Indels 34; Gaps 9;

RESULT 15
 A12656 angiotensin II receptor type 1B (AT3) - rat

N;Alternate names: angiotensin II receptor chain B
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C;Accession: A42656; S20423
 R;Sandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
 J.; Biol. Chem. 267, 9455-9458, 1992
 A;Title: Cloning and expression of a novel angiotensin II receptor subtype.
 A;Reference number: A42656; MUID:92250585; PMID:1374402
 A;Accession: A42656
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-359 <SAN>
 A;Cross-references: GB:M90065; NID:g202801; PID:AAA40704.1; PID:g202802
 A;Experimental source: adrenal cortex
 A;Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBITP:100268)
 R;Iwai, N.; Inagami, T.
 PEBS Lett. 298, 257-260, 1992
 A;Title: Identification of two subtypes in the rat type I angiotensin II receptor.
 A;Reference number: S20423; MUID:92183879; PMID:1544458
 A;Accession: S20423
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-359 <IWA>
 A;Cross-references: GB:X64052; NID:g57521; PID:CARA45410.1; PID:g57522
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 Query Match Score 3.9; DB 2; Length 359;
 Best Local Similarity 29.6%; Pred. No. 4.8e-20;
 Matches 92; Conservative 54; Mismatches 137; Indels 28; Gaps 10;
 Qy 26 VLFPLIYTVLFFVGLITNGL-AKRIFFQIRSKSNFIIPIKNTVISDLIMILPFPEKILSD 84
 Db 29 VMIPLYSITFVVGFGNSLIVVIVYFMMKLTAVSVELLNALADLCFLTIPLMNAVYT 88
 Qy 85 AKLGTCPLRTRFCVOTSVIIFTYTMISISFLGLITDRYOKTRPFKTSNPKNLIGAKIL 144
 Db 89 AMEYRWPPGHNLLKIASASVSNLYASVPLLTCISDRYLAIVHPMGSRRLRTMLYAKVT 148
 Qy 145 SVVIWAFMPLLSPMILTNQ-PRDKNPKKCSF-----LKSEFGLVWHEIVNYICQ 195
 Db 149 CIIIWIMAGLSPAVITYRNVYFTENTNTVCAHYEONSNTPIGLGLT-KNTLGKV-- 205
 Qy 196 VIFWINFLIVIVCYTLITKELYRSYVTRGVGKVRKVKVNVKF-IIIAV---PPICFVP 251
 Db 206 ---FPFLITLTSKLWALKKAYKIQK--NTPR--NDIFRIIMAIIVFFFWSWP 255
 Qy 252 FHFARIPIYTLSQTRDVFDCTAENTLYVKESTMNLTSNACLDPPFILCSFRNLSIS 311
 Db 256 HQITFLDVLJQLGTRDCEIADIVDTAMPITICIAVFNCNLNPFLYFLGKCFKRYFLQ 315
 Qy 312 MLK-CPNSATS 321
 Db 316 LKYIPTAKS 326

Search completed: February 4, 2004, 14:30:59
 Job time : 21 secs

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: February 4, 2004, 14:23:36 ; Search time 17 Seconds
(without alignments)
946.067 Million cell updates/sec

Title: US-09-780-576-2
Perfect score:
Sequence: 1 MQAVDNLTSAPGNTSLCTRDI.....SQDNRKKEQDGDPNEETPM 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SwissProt_41.1

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1778	100.0	342	1 P2YC_HUMAN	Q9h244 homo sapien
2	1748	98.3	342	1 P2YC_MACPA	Q95kc3 macaca fasci
3	1528.5	87.5	347	1 P2YC_MOUSE	Q9cpv9 mus musculus
4	1528.5	86.0	343	1 P2YC_RAT	Q9px4 rattus norvegicus
5	772	43.4	338	1 P2XX_HUMAN	Q15391 homo sapien
6	741.5	41.7	338	1 P2XX_MOUSE	Q9esg6 mus musculus
7	694	39.0	305	1 P2XX_RAT	Q35881 rattus norvegicus
8	488	27.4	319	1 H963_HUMAN	Q14626 homo sapien
9	411.5	23.1	375	1 GPB34_MOUSE	Q9rik6 mus musculus
10	409.5	23.0	381	1 GPB34_HUMAN	Q9upc5 homo sapien
11	394	22.2	342	1 PAFR_HUMAN	P25105 homo sapien
12	392.5	22.1	342	1 PAFR_CAVPO	P21556 cavia porcellus
13	379.5	21.3	361	1 EBI2_HUMAN	P32249 homo sapien
14	367	20.6	345	1 CLT2_PIG	Q95n03 sus scrofa
15	366	20.6	341	1 PAFR_MOUSE	Q62035 mus musculus
16	362	20.4	341	1 PAFR_RAT	P46002 rattus norvegicus
17	357.5	20.1	308	1 P2Y5_CHICK	P32250 gallus gallus
18	347.5	19.9	346	1 CLT2_HUMAN	Q9ns75 homo sapien
19	347.5	19.5	537	1 P2Y8_XENIA	P79928 xenopus laevis
20	344	19.3	309	1 CLT2_MOUSE	Q920a1 mus musculus
21	339.5	19.1	309	1 CLT2_PIG	Q924t9 rattus norvegicus
22	339	19.1	359	1 AG2R_BOVIN	P25104 bos taurus
23	338	19.0	344	1 P2Y5_HUMAN	P43657 homo sapien
24	334	18.8	359	1 AG2R_SHEEP	Q77590 ovis aries
25	334	18.8	367	1 GPI7_HUMAN	Q13304 homo sapien
26	329	18.5	359	1 AG2S_HUMAN	Q13725 homo sapien
27	328	18.4	340	1 CLTR1_PIG	Q95n02 sus scrofa
28	327	18.4	355	1 AG2R_PIG	P30555 sus scrofa
29	326	18.3	359	1 AG2R_CANPA	P43240 canis familiaris
30	325.5	18.3	399	1 PAR2_MOUSE	P55086 mus musculus
31	325	18.3	359	1 AG2R_RABBIT	P34976 oryctolagus cuniculus
32	321	18.1	359	1 AG2R_CAVPO	P30556 homo sapien
33	320	18.0	359	1 Q9wv26	cavia porcellus

ALIGNMENTS

RESULT 1	P2YC_HUMAN	STANDARD;	PRT;	342 AA.
ID	P2YC_HUMAN			
AC	Q9h244;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DB	P2Y Purinoreceptor 12 (P2Y12, (P2Y12 Platelet ADP receptor) (PPY (ADP)) (ADP-glycose receptor) (ADPG-R) (P2Y(AC)) (P2Y(cyc)) (P2T(AC)) (SPN999))			
DE	P2RY12 OR HKRG3.			
GN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21031966; PubMed=11196645; Hollópetter G., Jantzen H.-M., Vincent D., Li G., England L., RA Ranakrishnan V., Yang R.-B., Nurden P., Nurden A., Julius D.J., Conley P.B.; "Identification of the platelet ADP receptor targeted by anti-thrombotic drugs"; Nature 409:202-207 (2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Hypothalamus; MEDLINE=1264433; PubMed=11104774; Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X., Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M., Monsma P.J. Jr., RT SP1999 is the cognate ligand for the orphan G protein-coupled receptor			
RX	Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X., Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M., Monsma P.J. Jr., RT SP1999 is the cognate ligand for the orphan G protein-coupled receptor			
RA	Jin H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M., Monsma P.J. Jr., RT SP1999 is the cognate ligand for the orphan G protein-coupled receptor			
RX	SEQUENCE FROM N.A.			
RC	TISSUE-Brain; MEDLINE=121394281; PubMed=11502873; RA Takasaki J., Kamohara M., Saito T., Matsumoto S.-I., Ohishi T., Soga T., Matsubara H., Furuchi K., RT "Molecular cloning of the platelet P2T(AC) ADP receptor: pharmacological comparison with another ADP receptor, the P2Y11 receptor"; J. Biol. Chem. 276:8608-8615 (2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Brain; MEDLINE=121394281; PubMed=11502873; RA Takasaki J., Kamohara M., Saito T., Matsumoto S.-I., Ohishi T., Soga T., Matsubara H., Furuchi K., RT "Molecular cloning of the platelet P2T(AC) ADP receptor: pharmacological comparison with another ADP receptor, the P2Y11 receptor"; J. Biol. Chem. 276:8608-8615 (2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Reinschke R.K., Nothacker H.-P., Wang Z., Zeng J., Shihert F.J., Civelli O.; "ADP-glucose activates a G-protein coupled receptor and inhibits smooth muscle contractions," Submitted (Oct-2000) to the EMBL/GenBank/DDBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Takeda S., Kadowaki S., Haga T., Takeue H., Mitaku S.; "Identification of G protein-coupled receptor genes from the human genome sequence."			

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

[6] SEQUENCE FROM N.A.

RC TISSUE:Prostate;

RX MEDLINE=238827; PubMed=12477932;

RX STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RX Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Bhat N.K.,

RX Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Haleh F.,

RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Stapleton M., Soares M.B., Bondi M.F., Casavant T.L., Scheetz T.B.,

RX Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RX Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RX Bosak S.A., McEwan P.J., McErlean K.J.A., Malek J.A., Gunaratne P.H.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,

RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Fahey J., Helton E., Kerttunen M., Madan A., Rodriguez S., Sanchez A.,

RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RX Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RX Schneich A., Schein J.E., Jones S.J.M., Marras M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences."

RX Proc. Natl. Acad. Sci. U.S.A. 99:1699-1693 (2002)

CC !- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that inhibit the adenylyl cyclase second messenger system. Not activated by UDP and UTP. Involved in platelets aggregation.

CC |- SUBCELLULAR LOCATION: Integral membrane Protein.

CC |- TISSUE SPECIFICITY: Highly expressed in the platelets, lower levels in the brain. Lowest levels in the lung, appendix, pituitary and adrenal gland. Expressed in the spinal cord and in the fetal brain.

CC |- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: AF313449; AAC89444; -.

DR EMBL: AF3121815; AAC09484; -.

DR EMBL: AB02684; BAB0824; -.

DR EMBL: AF310685; AAL32292; -.

DR EMBL: AB033596; BAB89309; -.

DR EMBL: BC017898; AAH17898; -.

DR GenBank: HGNC:18324; F2RY12.

DR MIM: 600515; -.

DR CO: CO-007599; P:hemostasis; NAS.

DR InterPro: IPR00276; GPCR_Rhoopsin.

DR InterPro: IPR005394; P2Y12_Purinceptor.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPRHODOPN.

DR PROSITE: PS00231; G PROTEIN RECPT_F1_1; FALSE_NEG.

DR PROSITE: PS05026; G PROTEIN_RECPT_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN _1 25 EXTRACELLULAR second messenger system By

FT DOMAIN _1 25 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 26 46 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 47 58 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 59 79 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 80 99 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 100 120 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 121 142 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 143 163 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 164 191 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 192 212 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 213 233 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 234 254 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 255 281 EXTRACELLULAR (POTENTIAL).

	PT TRANSMEM	282	302	7 (POTENTIAL).
	PT DOMAIN	303	342	CYTOSOLIC (POTENTIAL).
	PT DISULFID	97	175	BY SIMILARITY.
	PT CARBOHYD	6	6	N-LINKED (GLCNAC, .) (POTENTIAL).
SQ SEQUENCE	13	13	N-LINKED (GLCNAC, .) (POTENTIAL).	
SQ SEQUENCE	342 AA:	39438 MW:	8553D2746C8176D CRC44;	
Qy	1 MQAVDNLTSA	100.0%	Score 1778; DB 1;	Length 342;
	Qy	Best Local Similarity	100.0%;	Pred. No. 3, 7e-17;
	Qy	Matches 342;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MQAVDNLTSA	100.0%	Score 1778; DB 1;	Length 342;
Db	1 MQAVDNLTSA	100.0%	Score 1778; DB 1;	Length 342;
Qy	61 IFLQNTVISDMLITFPKILSDAKLGTLPLRTFCVQTSVIFYFNMVISIFLGLITI	120	DRYQKTRPPKTSNPKNLGAKILSVVIAWFMLSLPEMLNTPRDNTKRCVNUKFSLRS	180
Db	61 IFLQNTVISDMLITFPKILSDAKLGTLPLRTFCVQTSVIFYFNMVISIFLGLITI	120	DRYQKTRPPKTSNPKNLGAKILSVVIAWFMLSLPEMLNTPRDNTKRCVNUKFSLRS	180
Qy	181 EFGLYWHETINYICQIVFWINLIVIVCYTLKELYLSYYRTRGVGRVPRKCVNUKF	240	181 EFGLYWHETINYICQIVFWINLIVIVCYTLKELYLSYYRTRGVGRVPRKCVNUKF	240
Db	181 EFGLYWHETINYICQIVFWINLIVIVCYTLKELYLSYYRTRGVGRVPRKCVNUKF	240	181 EFGLYWHETINYICQIVFWINLIVIVCYTLKELYLSYYRTRGVGRVPRKCVNUKF	240
Qy	241 IIAVFICFYPFHAFRIPYTLISQRDVFACTAENLYPKESTLWLTISLNACLDPEFYFP	300	241 IIAVFICFYPFHAFRIPYTLISQRDVFACTAENLYPKESTLWLTISLNACLDPEFYFP	300
Db	241 IIAVFICFYPFHAFRIPYTLISQRDVFACTAENLYPKESTLWLTISLNACLDPEFYFP	300	241 IIAVFICFYPFHAFRIPYTLISQRDVFACTAENLYPKESTLWLTISLNACLDPEFYFP	300
Qy	301 LCKSFNSLISMLKCPSNTSLSQDNRKCEQDGDPNEETPM	342	301 LCKSFNSLISMLKCPSNTSLSQDNRKCEQDGDPNEETPM	342
Db	301 LCKSFNSLISMLKCPSNTSLSQDNRKCEQDGDPNEETPM	342	301 LCKSFNSLISMLKCPSNTSLSQDNRKCEQDGDPNEETPM	342

RESULT 2

P2YC_MACFA

STANDARD;

PRT;

342 AA.

ID P2YC_MACFA

AC Q95KC3 ; QBGT8;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB P2Y Purinoceptor 12 (P2Y12).

GN P2Y12.

OS Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

OC Cercopithecinae; Macaca.

NCBI TaxID:9541;

RN SEQUENCE FROM N.A.

RC TISSUE=Frontal cortex, and Medulla oblongata;

RA Osada N.; Hida M.; Kusuda J.; Tanuma R.; Iseki K.; Hirai M.; Terao K.,

RA Suzuki Y.; Sugano S.; Hashimoto K.;

RA Isolation of full-length cDNA clones from macaque brain cDNA

RT Libraries.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that inhibit the adenylyl cyclase second messenger system. By

similarity.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR AB02684; BAB0824; -.

CC DR AF310685; AAL32292; -.

CC DR AF313449; AAC89444; -.

CC DR AF3121815; AAC09484; -.

CC DR AF313449; AAC89444; -.

DR EMBL; AB062981; BAB60747.1; -.

DR InterPro; IPR000376; GPCR_Rhodopsin.

DR InterPro; IPR005394; P2Y12_Purinocptor.

DR PRINTS; PRO0237; GPCR_HODOPSN.

DR PRINTS; PRO1569; P2Y12_PNCPTR.

DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.

DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1;

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 26 46 1 (POTENTIAL).

FT DOMAIN 47 58 CTOPLASMIC (POTENTIAL).

FT TRANSMEM 59 79 2 (POTENTIAL).

FT DOMAIN 80 99 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 100 120 3 (POTENTIAL).

FT DOMAIN 121 142 CTOPLASMIC (POTENTIAL).

FT TRANSMEM 143 163 4 (POTENTIAL).

FT DOMAIN 164 191 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 192 212 5 (POTENTIAL).

FT DOMAIN 213 233 CTOPLASMIC (POTENTIAL).

FT TRANSMEM 234 254 6 (POTENTIAL).

FT DOMAIN 255 281 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 282 302 7 (POTENTIAL).

FT DOMAIN 303 342 CTOPLASMIC (POTENTIAL).

FT DISULFID 97 175 BY SIMILARITY.

FT CARBOHYD 6 6 N-LINKED (GAGNAc . .) (POTENTIAL).

FT CARBOHYD 13 13 N-LINKED (GLCNAc . .) (POTENTIAL).

FT CONFLICT 49 49 I -> T (IN REF. 1; BAB33041).

FT CONFLICT 89 89 A -> T (IN REF. 1; BAB33041).

SQ SEQUENCE 342 AA; 33479 MW; E93FC62BFF5EBC4 CRC64;

Query Match Score 1748; DB 1; Length 342;

Best Local Similarity 98.3%; Score 1748; DB 1;

Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MQADNTSAGATSLCDRDXKIQTLQFLPLLLTFLVGLTNGLMALIPIQQRKSNSFI 60

Db 1 MQADNLNTSAGNTSLCDRDXKIQTLQFLPLLTFLVGLTNSLAMRIPIQRSNSFI 60

Qy 61 IFLKNTVTSIDLMLITLTPPKISLDAKLTGQPRTFVQQTWSVIFTYMSISIFGLITI 120

Db 61 IFLKNTVTSIDLMLITLTPPKISLDAKLTGAGAPRTFVQQTWSVIFTYMSISIFGLITI 120

Qy 121 DRYQKTRPFKTSNPKNLGAIIKLSVYTAWFLSLPNMILNRQPRDKVNRKCSFLKS 180

Db 121 DRYQKTRPFKTSNPKNLGAIIKLSVYTAWFLSLPNMILNRQPRDKVNRKCSFLKS 180

Qy 181 EFGLWHLIVNVIQCOVIFWINFVFLIVYCYTTLKELYRSYTRGTYGVPKRVNVKF 240

Db 181 EFGLWHLIVNVIQCOVIFWINFVFLIVYCYTTLKELYRSYTRGTYGVPKRVNVKF 240

Qy 241 IIAVFFICVPFHFAIRPYTLSQTRDVFCTAENTLYVKESTLWITSLNACLDPTIYFF 300

Db 241 IIAVFFICVPFHFAIRPYTLSQTRDVFCAENTLYVKESTLWITSLNACLDPTIYFF 300

Qy 301 LCKSFRNLSLISMILKCPNSATSLSQDNRKKEQQGGDPNEETPM 342

Db 301 LCKSFRNLSLISMILKCPNSATSLSQDNRKKEQQGGDPNEETPM 342

[1] RN SEQUENCE FROM N.A. TISSUE=Hippocampus, and Testis;
RC STRAIN=CS7BL/6J; PubMed=11217831;

RX MEDLINE=21088660; Pubmed=11217831;

RA Kavai J., Shinagawa A., Shiba T., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kondo H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
RA Saito T., Oizaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gasserland T., Gissel-Nielsen C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakaido J., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blaize J., Boffelli D., Botunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Built C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiyama M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringsdorf M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seye T., Shiba T., Storch K.-F.,
RA Suzuki H., Toyoko K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Kawaji H., Kohzuki S.,
RA Hayashiaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690 (2001).

[2] RN SEQUENCE FROM N.A. TISSUE=Hippocampus, and Testis;
RC STRAUSBERG R.L., FEINGOLD E.A., GROUSE L.H., DERGE J.G., SCHULER G.D., SHENMEN C.M., SCHULER G.D., SCHAFFER C.F., BHAT N.K., ALTSCHUL S.F., ZEEBERG B., BUELOU W.H., DERGE J.G., MAX S.I., WANG J., HSIEH F., HOPKINS R.L., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F., DIATCHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L., STEPLETON M., BONALDO M.P., CASAVANT T.J., CHEECHETZ T.E., BROWNSTEIN M.J., USDIN T.B., TOHYAMA K., CARMINCINI P., PRANGE C., RAHA S.S., LOQUELLANO N.A., PETERS G.J., ABRAMSON R.D., MULAHY S.J., BOAK S.A., MCLELLAN P.J., MCKERNAN J., MALEK J.A., GARNERATRE P.H., RICHARDS S., WORLEY K.C., HAILE S., GARCIA A.M., GAY L.J., RUYK S.W., VILLALON D.K., MUZZI D.M., SODERGREN E.J., LU X., GIBBS R.A., PALEY J., HELTON E., KETTERMAN M., MADAN A., RODRIGUES S., SANCHEZ A., WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., SOUFFARD G.G., BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C., RODRIGUEZ A.C., GRIMWOOD J., SCHMITZ J., MYERS R.M., BUTTERFIELD Y.S.N., KRZYWIŃSKI M.I., SKALSKA U., SMAILUS D.E., SCHNEIDER A., SCHEIN J.B., JONES S.J.M., MARRA M.A./ RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that inhibit the adenylyl cyclase second messenger system (By Simillarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; AB013804; BDB29000_1;

CC DR EMBL; AB014807; BDB29561_1;

CC DR EMBL; BC025428; ARH25428_1;

CC DR EMBL; BC027381; ARH27381_1;

CC DR MGD; MGI:1918089; P2RY12;

CC DR GO; GO:0005887; C: integral to plasma membrane; IC;

CC DR GO; GO:0001609; F: adenosine receptor, G-protein coupled activity; IMP.

CC DR GO; GO:0001621; P: platelet ADP receptor activity; IMP.

CC DR GO; GO:0007188; P: G-protein signaling, coupled to cAMP nucleic acid; IMP.

CC DR InterPro; IPR000236; GPCR_Rhodopsin.

CC DR InterPro; IPR005394; P2Y12_Purinocptor.

DR Pfam; PF00001; 7tm_1; 1;

DR PRINTS; PR00237; 'SPCRRHODOPSN.

DR PRINTS; PR1559; P2Y12PRNCPR.

DR PROSITE; PS00337; G PROTEIN RECEP F1_1; FALSE_NEG.

DR PROSITE; PS50062; G PROTEIN RECEP F1_2; 1;

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 31 52 . EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 53 64 . CYTOPLASMIC (POTENTIAL).

FT DOMAIN 65 85 . (POTENTIAL).

FT TRANSMEM 66 105 . EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 106 126 . (POTENTIAL).

FT DOMAIN 127 148 . CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 149 169 . (POTENTIAL).

FT DOMAIN 170 197 . EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 198 218 . (POTENTIAL).

FT DOMAIN 219 239 . CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 240 260 . (POTENTIAL).

FT DOMAIN 261 287 . EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 288 308 . (POTENTIAL).

FT DOMAIN 309 347 . CYTOPLASMIC (POTENTIAL).

FT DISULFID 103 181 BY SIMILARITY.

FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 12 12 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 3 3 V->M (IN REF. 2; AA05428).

SQ SEQUENCE 347 AA; 39473 MW; F107488E57B025F1 CRC64;

Query Match 87.5%; Score 1555.5; DB 1; Length 347;

Best Local Similarity 88.7%; Pred. No. 1.e-101;

Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

Qy 6 NLTSAPGNTSLCTRDYKTIQVLFPLLYTFVGLTINGLAMRIFFQIRSKENFIIFLKN 65

Db 12 NTTSPGTSTLVCPRYKTIQVLFPLLYTFVGLITLNSLARIFFQIQRSKENFIIFLKN 71

Qy 66 TVISPLMLTPEPKLSDAKLTGTGPLRTEFCVQTSVIFYFTMYIISTSEJGLITIIRYOK 125

Db 72 TVISPLMLTPEPKLSDAKLGAGPLPFLVQCVTSVIFYFTMYIISTSEJGLITIIRYKL 131

Qy 126 TTRPXTTSNPKNLGIKLSVIAWFMELLSLPNMLTNRQFDKNTYKKCPLKSBEFGLY 185

Db 132 TTRPXTSSSNLGIKLSVIAWFMELLSLPNMLTNRQFDKDTKCSPLKSEFGLY 191

Qy 186 WHEIINYICOIVFNFLIVCYTLKELLYSYVRGKVPRKVNTYKFIILAVF 245

Db 192 WHEIINYICOIVFNFLIVCYSLTKELLYSYVRGSKVPRKVNTYKFIILAVF 251

Qy 246 FICCPFPFHARIPIYTLSPQRDVFOCTAENTLTVKESTLWLTSLNACLDPPYFFLCKSF 305

Db 252 FICCPFPFHARIPIYTLSPQRDVFOCTAENTLTVKESTLWLTSLNACLDPPYFFLCKSF 311

Qy 306 RNSLISMLKPCNSATSLSDPNRKKEQDGDDPNBERTPM 342

Db 312 RNSLTSMLRSNS-TSTSGTNKKQGEQEGPSSETPM 347

RESULT 4

P2YC RAT STANDARD; PROT; 343 AA.

ID P2YC RAT STANDARD; PROT; 343 AA.

AC Q9EXX4; (Rel. 41, Created)

DT 28-Feb-2003 (Rel. 41, Last sequence update)

DT 28-Feb-2003 (Rel. 41, Last annotation update)

DE P2Y_purinoreceptor_12 (P2Y12 platelet ADP receptor).

GN P2Y12.

CS Ratetus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Buteraria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=21037366; PubMed=1119645;

RA Hollopeter G, Jantzen H.-M., Vincent D, Li G., England L.,

RA Ramakrishnan V., Yang R.-B., Nurden P., Nurden A., Julius D.J.,

RA Conley P.B.;

RT "Identification of the platelet ADP receptor targeted by antithrombotic drugs."

RT Nature 409:202-207(2001).

RL -; FUNCTION: Receptor for ADP and ATP coupled to G-proteins that inhibit the adenylyl cyclase second messenger system (By similarity).

CC -; SUBCELLULAR LOCATION: Integral membrane protein.

CC -; SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -; DR InterPro; IPR00216; GPCR_Rhodopsin.

CC -; DR InterPro; IPR005394; P2Y12_Purinceptor.

CC -; DR PRINTS; PR00237; GPCR_RHODOPEN.

CC -; DR PRINTS; PR01569; P2Y12_PRNCPR.

CC -; DR PROSITE; PS00337; G-PROTEIN_RECCEP_F1_2; 1; FALSE_NEG.

CC -; DR PROSITE; PS50062; G-PROTEIN_RECCEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 32 52 1 (POTENTIAL).

FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 65 85 2 (POTENTIAL).

FT DOMAIN 86 105 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 106 126 3 (POTENTIAL).

FT DOMAIN 127 148 4 (POTENTIAL).

FT DOMAIN 170 197 5 (POTENTIAL).

FT DOMAIN 219 239 6 (POTENTIAL).

FT DOMAIN 240 260 7 (POTENTIAL).

FT DOMAIN 261 287 8 (POTENTIAL).

FT DOMAIN 288 308 9 (POTENTIAL).

FT DOMAIN 309 347 10 (POTENTIAL).

FT DOMAIN 312 343 AA; 39047 MW; TAE0A0E66674136 CRG64;

Query Match 86.0%; Score 1528.5; DB 1; Length 343;

Best Local Similarity 86.9%; Pred. No. 8.e-100;

Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

Qy 6 NLTSAPGNTSLCTRDYKTIQVLFPLLYTFVGLTINGLAMRIFFQIRSKENFIIFLKN 65

Db 12 NTTSPLPTLCSDYKTIQVLFPLLYTFVGLITLNSLARIFFQIQRSKENFIIFLKN 71

Qy 66 TVISPLMLTPEPKLSDAKLTGTGPLRTEFCVQTSVIFYFTMYIISTSEJGLITIIRYOK 125

Db 72 TVISPLMLTPEPKLSDAKLGAGPLPFLVQCVTSVIFYFTMYIISTSEJGLITIIRYKL 131

Qy 126 TTRPXTTSNPKNLGIKLSVIAWFMELLSLPNMLTNRQFDKNTYKKCPLKSBEFGLY 185

Db 132 TTRPXTSSSNLGIKLSVIAWFMELLSLPNMLTNRQFDKDTKCSPLKSEFGLY 191

Qy 186 WHEIINYICOIVFNFLIVCYTLKELLYSYVRGKVPRKVNTYKFIILAVF 245

Db 192 WHEIINYICOIVFNFLIVCYSLTKELLYSYVRGSKVPRKVNTYKFIILAVF 251

Qy 246 FICCPFPFHARIPIYTLSPQRDVFOCTAENTLTVKESTLWLTSLNACLDPPYFFLCKSF 305

Db 252 FICCPFPFHARIPIYTLSPQRDVFOCTAENTLTVKESTLWLTSLNACLDPPYFFLCKSF 311

Qy 306 RNSLISMLKPCNSATSLSDPNRKKEQDGDDPNBERTPM 342

Db 312 RNSLTSMLRSNS-TSTSGTNKKQGEQEGPSSETPM 347

Qy 306 WHEIINYICOIVFNFLIVCYTLKELLYSYVRGKVPRKVNTYKFIILAVF 245

Db 192 WHEIINYICOIVFNFLIVCYSLTKELLYSYVRGSKVPRKVNTYKFIILAVF 251

Qy 126 TTRPXTTSNPKNLGIKLSVIAWFMELLSLPNMLTNRQFDKNTYKKCPLKSBEFGLY 185

Db 132 TTRPXTSSSNLGIKLSVIAWFMELLSLPNMLTNRQFDKDTKCSPLKSEFGLY 191

QY	306 RNSLISMLKCPNSATSLSDNRNKKEDGGDPNBBTPM 342	PRINTS; PRO0237; GPCRBDODPSN.
Db	312 RNSLISMLR-----STSGANCKGQEGDPSEETPM 343	DR PRINTS; PR0165; UDPGLUCOSE.
		DR PROSITE; PS0237; G PROTEIN RECEP F1.1; FALSE_NEG.
		DR PROSITE; PS50262; G PROTEIN RECEP F1.2; 1.
		G-protein coupled receptor; Transmembrane; Glycoprotein.
RESULT 5		
P2YX HUMAN STANDARD;	PRT; 338 AA.	
ID P2YX_HUMAN		
AC Q15351;		1 (POTENTIAL).
DT 15-JUL-1998 (Rel. 36 , Created)		CYTOSMIC (POTENTIAL).
DT 15-JUL-1998 (Rel. 36 , Last sequence update)		2 (EXTRACELLULAR (POTENTIAL).
DT 28-FEB-2003 (Rel. 41 , Last annotation update)		EXTRACELLULAR (POTENTIAL).
DE UDP-Glucose receptor (G protein-coupled receptor GPR105).		3 (POTENTIAL).
GN GPR105 OR KIAA0001		CYTOSMIC (POTENTIAL).
OS Homo sapiens (Human)		4 (POTENTIAL).
OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		EXTRACELLULAR (POTENTIAL).
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		5 (POTENTIAL).
OX NCBI_TaxID:9506;		CYTOSMIC (POTENTIAL).
RN [1]		6 (EXTRACELLULAR (POTENTIAL).
RC TISSUE=Bone marrow.		7 (POTENTIAL).
RX MEDLINE=9051337; PubMed=7584026;		CYTOSMIC (POTENTIAL).
RX MEDLINE=9051337; PubMed=7584026;		BY SIMILARITY.
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,		N-LINKED (GLCNAC . .) (POTENTIAL).
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.,		3 (POTENTIAL).
RA "Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA001-KIAA040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1"; DNA Res. 1:27-35(1994).		4 (POTENTIAL).
RN [2]		161 161 N-LINKED (GLCNAC . .) (POTENTIAL).
RP SEQUENCE FROM N.A.		338 AA; 38971 MW; 8DBE7C782CB4753D CRC34;
RC TISSUE=Bone marrow.		Score 772; DB 1; Length 338;
RA "Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA001-KIAA040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1"; DNA Res. 1:27-35(1994).		Best Local Similarity 47.5%; Pred. No. 3_9e-47;
RT Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;		Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;
Qy 6 NLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFGLTINGLQLRKIFQRSKRNFLIFRN 65		
Db 3 NSTSTOPPDESCQNLLITQIIPVLYCMVFLIGILNGSMIFPFYSSSPITILKN 62		
Qy 66 TVISDLMLMTPEPKILSDAKLGTGPARTFCVOTTSVLYFTMYTISISFLGLITDRYK 125		
Db 63 TVIADETMWSLTFPPKILGSGLGPWQLNVFCVRSAVLYVNNNVSIVFGLISFDRYK 122		
Qy 126 TTTRPKTSNPKNLGAKILSVVIAEMPLSLSPNMILTNQPDKVNCKCSFLKSBEFGIV 185		
Db 123 IVKCPWNTSFQSYSKLISVIVMLLAVNVLITNQSREVTQIKCIEURGEIURK 182		
Qy 186 WHEITVNYICQVTFINFLIVVYCYTLKELYSVYTRGVYVPRKVNVKFVILLAY 245		
Db 183 WHKASNYIYPAIWFVNLIVVYTAIKTKFHKSHLKSRSRNSTSVKCKSRSNFISIVFV 242		
Qy 246 FICCFYPPHFAPIPTLQSQDVFCTAINTLTYKESTWLWLTSLNACDPPFYFLCKSF 305		
Db 243 FVCCFPYHAIPIPTKSKOEAHYSCQSKILRNKEFTLLSRAVNCUDPLYFFFLCQP 302		
Qy 306 RNLSLIMLKCPNSA 319		
Db 303 RETLCKKLHPLKA 316		
RESULT 6		
P2YX_MOUSE STANDARD; PRT; 338 AA.		
ID P2YX_MOUSE		
AC Q9ES05		
DT 28-FEB-2003 (Rel. 41 , Created)		
DT 28-FEB-2003 (Rel. 41 , Last sequence update)		
DT 28-FEB-2003 (Rel. 41 , Last annotation update)		
DE UDP-glucose receptor (G protein-coupled receptor GPR105).		
GN GPR105		
OS Mus musculus (Mouse)		
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; OX NCBI_TaxID:10090;		
RP SEQUENCE FROM N.A.		[1]
RA Lee B.C., Scadden D.T./ "7 transmembrane G protein coupled receptor from hematopoietic progenitors"; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.		
DR EMBL; D13626; BAA02791.1; -.		
DR EMBL; AF046925; AAL4764.1; -.		
DR Genev; HGNC:16442; GPR105.		
DR GO: GO:0016021; C:integral to membrane; NAS.		
DR GO: GO:005029; P:G-activated nucleotide receptor activity; NAS.		
DR GO: GO:007186; P:G-protein coupled receptor protein signalin.. . ; NAS.		
DR InterPro; IPR000276; GPCR_Rhodopsin.		
DR InterPro; IPR005466; UDPG_receptor.		
DR Pfam; PF00001; 7tm_1; 1.		

Page 6

- - FUNCTION: Receptor for UDP-glucose coupled to G-proteins (By similarity).

- - SUBCELLULAR LOCATION: Integral membrane protein.

- - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; API17711; AAG09275.1; -.

 | M67; MG1:2157505; Gpr105.

 | GO; GO:0016021; C:integral to membrane; ISS.

 | GO; GO:0145039; F:UDP-activated nucleotide receptor activity; ISS.

 | GO; GO:0007846; P:G-protein coupled receptor protein signalin. . .; ISS.

 | InterPro; IPR000276; GPCR_Rhodopsin.

 | InterPro; IPR005466; UDPG_Receptor.

 | Pfam; PF00001; 7tm_1; 1.

 | PRINTS; PRO0123; GPCR_RHODOPN.

 | PRINTS; PS00237; G_protein_recep_F1_1; FALSE_NEG.

 | PROSITE; PSS0262; G_protein_recep_F1_2; 1.

 | G_protein_coupled_receptor; Transmembrane; Glycoprotein.

 | DOMAIN; 1; 29; EXTRACELLULAR (POTENTIAL).

 | TRANSMEM; 30; 50; EXTRACELLULAR (POTENTIAL).

 | DOMAIN; 51; 55; CYTOPLASMIC (POTENTIAL).

 | TRANSMEM; 56; 76; CYTOPLASMIC (POTENTIAL).

 | DOMAIN; 77; 96; EXTRACELLULAR (POTENTIAL).

 | TRANSMEM; 97; 117; 3 (POTENTIAL).

 | DOMAIN; 118; 139; CYTOPLASMIC (POTENTIAL).

 | TRANSMEM; 140; 160; 4 (POTENTIAL).

 | DOMAIN; 161; 188; EXTRACELLULAR (POTENTIAL).

 | TRANSMEM; 189; 209; CYTOPLASMIC (POTENTIAL).

 | DOMAIN; 210; 234; EXTRACELLULAR (POTENTIAL).

 | TRANSMEM; 235; 255; 6 (POTENTIAL).

 | DOMAIN; 256; 278; EXTRACELLULAR (POTENTIAL).

 | TRANSMEM; 279; 299; 7 (POTENTIAL).

 | DOMAIN; 300; 338; CYTOPLASMIC (POTENTIAL).

 | DISULFID; 94; 172; BY SIMILARITY.

 | CARBOHYD; 2; 2; N-LINKED (GLCNAC. . .) (POTENTIAL).

 | CARBOHYD; 3; 3; N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE; 338 AA; 38861 MW; 437650622A68A4E CRC64;

Query Match Score 741.5; DB 1; Length 338;
Best Local Similarity 44.1%; Pred. No. 5.1e-45; Indels 7; Gaps 3;

Y	4 VDNLTSAAGNTSLCTRDYKITLVLFPLLYTVLFFVGLTINGLAMRIFFQIRSKNSNFIIFL 63
o	1 MNNTSTIDPENQPCWNTLITKQIIPFLGGLINGLWIFVPPSKPSKSFY 60
o	64 KNTIVSDLMILTFPKISDAKGTPGSPRTIVCQVTSVIFPTMVISFGLITIIRR 123
o	61 KNIVVADFLMGLTFFPKLGDSLGPWQVNFVCVRVSAYFVYNNMVSVFFGIGSFDRY 120
o	124 QKTRPEKTSNPKNLGAKLSVWTAWFMLLSLENMILMTNRQPRDKTKCSFLKSEFG 183
c	121 YKIVPPLLSIVQSYKNSKLLVWMMMLLAFLVIIITNGTYKEVTKIQCMELKNEV 180
o	184 LVMHIVNTIVQIVPFWINFLIVTYCYTLLTKELYRSYVTRGVCKVPRCKVNTKVFLIA 243
c	181 RKWHAASNYFVSFWVFLLIVYTAITRKFLSHLKSRSNTVKRSNSRNFNSIVL 240
o	244 VFFIEVPHFPHARTYPTISLQTRDFTCAENTLYVKEKSTMLTSINAUDPETYFLICK 303
c	241 VFFFVFPVTHYARIYVTKSCRGHTSCTRIVTLLYAKEFTILLUSAANYCUDPITYFLCQ 300
o	304 SFR--NSLISM-LCPNSATSLSDNRKE 330
c	301 PEREVNKKHMSKRYVON--DDEYSKTRKE 328

RESULT 7	P2YX RAT	PRT;	305 AA.
AC	O35811; ID P2YX RAT	STANDARD;	
DT	15-JUL-1998 (Rel. 36; Created)	PRT;	
DT	15-JUL-1998 (Rel. 36; Last sequence update)		
DT	15-JUL-2003 (Rel. 42; Last annotation update)		
DR	UDP-Glucose receptor (G protein-coupled receptor GPR105) (VTR 15-20).		
GN	GPR105.		
OS	Rattus norvegicus (Rat).		
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.		
OX	NCBI_TAXID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MedlineID=9295203; PubMed=1439647;		
RA	Charlton M.E., Williams A.S., Fogliano M., Sweetnam P.M., Duman R.S.:		
RT	"The isolation and characterization of a novel G protein-coupled receptor regulated by immunologic challenge."		
RT	Brain Res. 764:141-148 (1997).		
RL	-1- FUNCTION: Receptor for UDP-glucose coupled to G-proteins (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	CC DR U76206; #AB71745; -		
DR	GO; GO:0016021; C:Integral to membrane; ISS.		
DR	GO; GO:005029; F:UDP-activated nucleotide receptor activity; ISS.		
DR	GO; GO:0007186; P:G-Protein coupled receptor protein signalin. . . ; ISS.		
DR	InterPro; IPR00276; GPRC_Rhodopsn.		
DR	IntProEl; IPRE05466; UDPG_Receptor.		
DR	PFam; PF00001; ttm_1; 1.		
DR	PRINTS; PRO00237; GCBRHODOPSN.		
DR	PRINTS; PRO1655; UDPGLUCOSER.		
DR	PROSITE; PS00027; G PROTEIN RECEP_F1_1; FALSE NEG.		
KW	G-protein coupled receptor; Glycoprotein.		
FT	DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 30 50 1 (POTENTIAL).		
FT	TRANSMEM 51 55 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 56 76 2 (POTENTIAL).		
FT	DOMAIN 77 96 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 97 117 3 (POTENTIAL).		
FT	DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 140 160 4 (POTENTIAL).		
FT	TRANSMEM 161 188 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 189 209 5 (POTENTIAL).		
FT	DOMAIN 210 234 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 235 255 6 (POTENTIAL).		
FT	DOMAIN 255 278 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 279 299 7 (POTENTIAL).		
FT	TRANSMEM 300 305 CYTOPLASMIC (POTENTIAL).		
FT	CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBONYD 161 160 N-LINKED (GLCNAC. . .) (POTENTIAL).		
SQ	SEQUENCE 34800 MW; 640046A68ECC7A3 CRC64;		
Query Match	39.0%	Score 694;	DB 1;
Best Local Similarity	45.2%	Pred. No. 9.5e-42;	
Matches 132;	Conservative 61;	Mismatches 99;	Indels 0;
Gaps	0;		

Y	64	KNTVSDLMLTTPFKILSDAXGTGPLRTFVCQVTSTVIFYFTMMYISISFLGLITIDRY	123
O	61	KNIVADFGMLTTPFKVLSDGIGPQUNVVFYERAVTFYNNMYYSTAFFGIGIS	120
Y	124	QKTTPRPEKTSNPKNLJGAKLISVWAFMELISPMILITNORPRDKVKKCSPIKSFG	183
O	121	YKIVRPLIYSIVSYNSKVLSLVWMLLLAVPNILITNOSVYDVTNIQCMELKNELG	180
Y	184	LWHEEIVNVIQVIFWINELIVCYTLLTKELYSYVTRGKVPRKVKVTFIIIA	243
O	181	RKHKASVYEVSVWIVLWLYFYMATAKFKHSKRNSISVVKSESSNFSTV	240
Y	244	VFFICVFPPFHARIPPTYLSQLRDYFDCTAENTLYVKESTLWLTSLNACLDP	295
O	241	AFACAFAPPHVARIPPTYSQTEGHISQCQKETLLYTKETFLUSAANYCLDP	292

RESULT 8

H963_HUMAN	STANDARD;	PRT;	319 AA.
Q_104676;			
O104676;	(Rel. 39, Created)		
O104676;	30-MAY-2000 (Rel. 39, Last sequence update)		
O104676;	30-MAY-2000 (Rel. 41, Last annotation update)		
O104676;	28-FEB-2003 (Rel. 41, Last annotation update)		
O104676;	Probable G protein-coupled receptor H963.		
Homo sapiens (Human).			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
Metazoa; Craniata; Vertebrata; Euteleostomi;			
Eukaryota; Metazoa; Chordata;			
[1] NCBI_TaxID=9606;			
SEQUENCE FROM N.A.			
TISSUE=peripheral blood monocytes;			
MEDLINE=98036061; PubMed=9372294;			
Jacobs K.A., Collins-Racie L.A., Colbert M.J., Duckett M.,			
Golden-Fleet M., Kelleher K., Kriz R., Lawrence E.R., Marberg D.,			
Spaulding V., Stover J., Williamson M.J., McCoy J.M.;			
[2] A Genetic selection for isolating cDNAs encoding secreted proteins.;			
Carroll 100(2002)202-207.			

[2] SEQUENCE FROM N.A.; PubMed-11524702;
MEDLINE-21426338; Jonsuu T., Haemalaainen R., Yuan B., Johnson C., Tegelberg S., Gasparini P., Zeilante L., Pirvola U., Pakarinen L., Lehesjoki A.-E., de la Chapelle A., Santtila E.-M.; "Mutations in a novel gene with transmembrane domains underlie Usher syndrome type 3." Am. J. Hum. Genet. 69:673-684 (2001).
-1 : FUNCTION: ORPHAN RECEPTOR.
-1 : SUBCELLULAR LOCATION: Integral membrane protein.
-1 : SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announce>).

or send an email to license@sb-lib.ch.

```

EMBL; AE002986; AAC51846.1; -.
EMBL; AF411849; AF411850; -.
EMBL; GO:0016201; C-integral to membrane; NAS.
GO; GO:0007186; PIG-protein coupled receptor protein signalin. . ; NAS.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1._PRINTS;
PR00237; G_CGRRHDOPSN.
PROSITE; PS00037; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50062; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor_Transmembrane; Glycoprotein.
DOMAIN; 1; 21; EXTRACELLULAR ( POTENTIAL ) .
TRANSMEM; 22; 42; 1_BONDENTAT

```

FT	DOMAIN	4	3	48	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	4	9	69	2 (POTENTIAL).
PT	DOMAIN	7	0	89	EXTRACELLULAR (POTENTIAL).
PT	TRANSMEM	9	0	110	3 (POTENTIAL).
PT	DOMAIN	11	1	132	CYTOPLASMIC (POTENTIAL).
PT	TRANSMEM	13	3	153	4 (POTENTIAL).
PT	DOMAIN	15	4	181	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	18	2	202	5 (POTENTIAL).
PT	DOMAIN	20	3	224	CYTOPLASMIC (POTENTIAL).
PT	TRANSMEM	22	5	245	6 (POTENTIAL).
PT	DOMAIN	24	6	268	EXTRACELLULAR (POTENTIAL).
PT	TRANSMEM	26	9	289	7 (POTENTIAL).
FT	DOMAIN	29	0	319	CYTOPLASMIC (POTENTIAL).
FT	CARBONYD	3	3	344	N-LINED (GLCNAC ⁻) (POTENTIAL).
SQ	SEQBONDCE	319	AA:	36754	MW: 7938921C1084114 CRC64;
Query Match		27.4%		Score 488;	DB 1;
Best Local Similarity		34.5%		Pred. No. 2.2e-27;	
Matches	112;	Conservative	62;	Missmatches	125;
				Indels	26;
				Gaps	9;
Qy	13 NTSLCTRDYKIQVQLPFLPLVYLTFPFVCLITGLAMRIFFQITRSKSNIPI-IFLKNTVISDL	71			
Db	3 NSSPFPCPVYKDLEP-TFTYFVLPGLGSCPATWAFIQNTENFCRVSIVYLINLTIDP	61			
Qy	72 LMLTLPFKILSALKLGTGP--LRTFVQCVTSVIFVFTMVISIISITGLIITDRVQTKTRP	129			
Db	62 LLTLLAPVXIVD--LGVAPWKLKITHFCVTAFLCYTINMYLISITIPLAFAVSTDRCLQLOTHS	119			
Qy	130 FKTSNPKNLGAKILSVVYIWATMFLSLPNMLTINSPQRDKNVKKSFLKFSEGLVWHETI	189			
Db	120 CKYRIOQEGBGPAMISTVWTMVLIMVNMNMPIDTIKEKSNVSGOMEPEKEFGRWHL	179			
Qy	190 VNTICQVIFWNV-LIVIVCVTLLTGYLSRYTGVGVYPR-KRVNTVVFIIATVFFI	247			
Db	180 TNFICVAV-F-INFSAVLLISNLVIRLYRN---KDNENYTPVVKALNILLVTVGYI	234			
Qy	248 CFPFHFARIPTVPLSQTSDVDFCTATNTLFYKTESTLWTLSLNACIDPFFYFFFLCKSFRN	307			
Db	235 CFVPHIVRIPYPLSQTETVITOSCTRISLFLKAREATLILLAVSNLCEDPFLVYHLSKAFRS	294			
Qy	308 SLI-----SMLKCPNSA	319			
Db	295 KVTEFASFASPKETKAQKERKLRNNA	319			
RESULT 9					
GP34_MOUSE					
ID GP34_MOUSE					
AC Q9R4K6;					
PR STANDARD;					
PRT					
375 AA.					
RN [1]					
RP SEQUENCE FROM N.A.					
RA MEDLINE-#93326137; PubMed=10395919;					
RA Schoneberg F., Schulz A., Grosse R., Schade B., Henklein P.,					
RA Schultz G., Gudermann T.;					
RT "A novel subgroup of class I G-protein-coupled receptors.";					
RL Biochim Biophys Acta 1446:57-70(1999).					
CC -1- FUNCTION: ORPHAN RECEPTOR.					
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).					
CC -1- TISSUE/SPECIFICITY: BROADLY EXPRESSED.					
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -					
CC					

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).

CC	GN	GPR34.
CC	OS	<i>Homo sapiens</i> (Human).
CC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CC	NCBI_TAXID	9606;
DR	RN	[1] _
DR	RP	SEQUENCE FROM N.A.
DR	RC	TISSUE=fetal brain;
DR	RX	Medline=93026137; PubMed=10395919;
DR	RA	Schoneberg T., Schulz A., Grosse R., Schade R., Henklein P.,
DR	RA	Schultz G., Gudermann T.;
DR	RA	"A novel subgroup of class I G-protein-coupled receptors.";
DR	RL	Biochim. Biophys. Acta 1446:57-70(1999).
DR	RN	[2]
DR	RP	SEQUENCE FROM N.A.
DR	RX	Medline=91156152; PubMed=10036181;
DR	RA	Marchese A., Sawardjorg M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
DR	RA	Im D.-S., Lynch K.R., George S.R., O'Dowd B.F.;
XW	RT	"Discovery of three novel orphan G-protein-coupled receptors.";
Receptor; G-protein coupled receptor; Transmembrane Glycoprotein.	RL	Genomics 56:12-21(1999).
XW	RN	[3]
FT	RN	SEQUENCE FROM N.A.
TRANSMEM DOMAIN 1	RX	Medline=20434221; PubMed=10982042;
FT	RA	Jacobi F.K., Brogammer M., Pesch K., Zrenner B., Berger W.,
TRANSMEM DOMAIN 1	RA	Meindl A., Pusch C.M.;
FT	RA	"Physical mapping and exclusion of GPR34 as the causative gene for congenital stationary night blindness type 1.";
TRANSMEM DOMAIN 1	RT	Genomics 56:12-21(1999).
FT	RN	[4]
TRANSMEM DOMAIN 1	RX	SEQUENCE FROM N.A.
FT	RA	Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Oshima A.;
TRANSMEM DOMAIN 1	RA	"NEDO human cDNA sequencing project.";
TRANSMEM DOMAIN 1	RA	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
FT	RN	[5]
DISUFID	RP	SEQUENCE FROM N.A.
CARBODY	RX	Medline=23388257; PubMed=12477932;
CARBODY	RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaeffer C.F.P., Bhat N.K., Altschul S.P., Zeeberg B., Buetow K.H., Wang J., Hsieh F., Hopkins R.F., Jordan R., Moore T., Max S.E., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Diatchenko L., Soares M.B., Ronald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., Peterman K.J., Malek J.A., Gunaratne P.H., Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Keittman M., Madan A., Rodriguez S., Sanchez A., Whiting N., Madan A., Young A.C., Shcherbina Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.B., Jones S.J.M., Marr M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
CARBODY	RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CARBODY	CC	- - FUNCTION: ORPHAN RECEPTOR.
CARBODY	CC	- - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CARBODY	CC	- - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
SEQUENCE	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/).
QY	2	DAVDNITSAGNTSLCTRDYKIQVLFPLVLYTVLFFVGLITNGIAMRIFQFRSKNSFEL- 60
Db	25	QASQNFSQGPVNTS-CPMDEKLLSLVLTTFYSVTFVGLVNTIALTYFLGHRKRSIQ 83
QY	61	IPLKNTVISDILMILTEPFKILSDAKLGTCPLRFVQCVTSVIFYFIMVISFGLHTI 120
Db	84	IYLLAYAVADLLIFCLPFPKMYHNQNKWTLGTVLCKVGTFLFYMMYNTISILLGPDSL 143
Qy	121	DRYQKTRPFTPSNPKNLQAKNLQSVVIAWFMLSLSPNMLNRPQDQTKVKKCSFLKS 180
Db	144	DRYIKNRNSIGQRRAITKQSYIVCIVWT- VALAGFLTMILTLKKGHNSTMCFHYRD 202
Qy	181	BFGLVWHEIVYIVQYIFWFLNFLIVTVCLTLYR-SYVRTR--GVGKVBRKKVVK 237
Db	203	RHNAKGEAIPFVLVUMFLFLILSITKIGNLLRISKRSKEPNSGKVTATTN- 260
Qy	238	VFIILAVFFCIFVFPHFAR-LPFYLTSQTRDYFDCTAENTFLYKESTLWLTSNACLDPFI 297
Db	261	SFIVLIFTICFVPHAFRFFYISSL-NVSCYKREIHTNEIMLVFSSFNCLDFVM 319
Qy	298	YFFFLCKSFERNLISML 313
Db	320	YFLMSSNIRKIMCQLL 335
RESULT 10		
GP34_HUMAN	ID	GP34_HUMAN STANDARD;
GP34_HUMAN	AC	Q9UPC5; OS9853;
GP34_HUMAN	DT	16-Oct-2001 (Rel. 40, Created)
GP34_HUMAN	DT	16-Oct-2001 (Rel. 40, Last sequence update)
GP34_HUMAN	DT	15-Sep-2003 (Rel. 42, Last annotation update)
DE	DE	Probable G protein-coupled receptor GPR34.

or send an email to license@ibsh-sib.ch).

CC DT 01-MAY-1992 (Rel. 22, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR DE Platelet activating factor receptor (PAFR).
 EMBL GN
 EMBL: AF039616; AAD50311.; -.
 EMBL: AF118670; AAD17481.; -.
 EMBL: BML770; BAB55321.; -.
 EMBL: BC020678; AAH205781.; -.
 Genew: HGNC:4490; GPR34.
 MIM: 300241.; -.
 DR GO: GO:0005886; C:integral to plasma membrane; P:G-protein coupled receptor protein signalin.. . ; TAS.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin.. . ; TAS.
 DR InterPro: IPR00276; SPCR_Rhodopsin.
 DR PFam: PF00001; Tern1.; 1.
 PRINTS: PRO0237; GPCRCHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECGBP_F1_1.; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECGBP_F1_2.; 1.
 DR Receptor: G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW FT DOMAIN 1 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 61 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 62 1 (POTENTIAL).
 FT DOMAIN 83 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 89 109 2 (POTENTIAL).
 FT DOMAIN 110 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 3 (POTENTIAL).
 FT DOMAIN 150 171 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 172 192 4 (POTENTIAL).
 FT DOMAIN 193 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 237 5 (POTENTIAL).
 FT DOMAIN 238 269 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 270 290 6 (POTENTIAL).
 FT DOMAIN 291 310 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 311 331 7 (POTENTIAL).
 FT DOMAIN 332 381 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 127 204 BY SIMILARITY.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CONFLICT 181 181 L -> V (IN REF. 1).
 SQ SEQUENCE 381 AA: 43860 MW: 491FC016E5624379 CRG64;
 Query Match 23.0%; Score 409.5; DB 1; Length 381;
 Best Local Similarity 32.3%; Pred. No. 7.e-22;
 Matches 102; Conservatve 53; Mismatches 152; Indels 9; Gaps 7;

QY 2 QAVDNLTSAPGNTSLCTRDYKIQTQLQFLPVLYTVLFPVGLITGLANRIFQRSKSNFI- 60
 Db 32 QPPQNFSATP-NVTPCPMDKLSLSTVLTSYSVIIVGLGVNIALXVFLGHKRKNSQ 90
 Qy 61 IFLKNTVISDLMLTFPEPKLSDAKLGTPRTFCVOTYTFYFTMYIS-SFLGHTI 120
 Db 91 YIYNLVAIADLFLCLPRTMHNQKWTGLVILCKVGYFLYNNMYSILLGPISL 150
 Qy 121 DRYOKTTRPEKTSNPKNLGAKLSSWVIAFPMLSLPNMILTNRPRDKNTVKCSPLKS 180
 Db 151 DRYIKINRSLQRKAITKQSTIVCCIW-MLAQGFLTMILTLKGGANSTMCFHYRD 209
 Qy 181 EFGLYWHEIVNYCQVIFWNEFLIVIVCYCTLTKELYR-SYVRTR--GVGKVPRKCVNK 237
 Db 210 KHNARGEAIFNFILVMMFLILSYIKGNLRISKRSKFPNSGKATTARN-- 267
 Qy 238 VFTIAVAPPFCVUPFHARIPIYLSQTDFDCTAENTLFYKESTIWLTSINAQCDPFI 297
 Db 268 SFIVLIIIFTFCVBYHAFFTYISSLQ-NVSSCYKEIVHKTEIMLVLSSTSNSCLDPVM 326
 Qy 298 YFFLCKSFNSLISM 313
 Db 327 YFLMSSNIKMCQIL 342

RESULT 11
 PAFR_HUMAN ID STANDARD; PRT; 342 AA.
 ID PAFR_HUMAN STANDARD; PRT; 342 AA.

RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander Z.S.; Nat. Genet. 23:373-373 (1999).

CC -|- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOPTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: M8674; AAA60001.1; DR EMBL: M76674; AAA60002.1; DR EMBL: D10002; BAA01050.1; DR EMBL: M88177; AAA6014.1; DR EMBL: S52242; AAB24695.2; DR EMBL: L07334; AAA60108.1; DR EMBL: S56196; AAB25155.1; DR PIR: A4011; A40191.1; DR GENB: H9582; PTAFR. NMIM: 173335; DR GO: GO:0005887; C:integral to plasma membrane; TAS. DR GO: GO:0004992; F:Platelet activating factor receptor activity; TAS. DR GO: GO:0006960; P:Antimicrobial humoral response (sensu lato); TAS. DR GO: GO:0006935; P:Chemotaxis; TAS. DR GO: GO:0007186; P:G-protein coupled receptor protein signalin.; .; TAS. DR GO: GO:0006955; P:Immune response; TAS. DR GO: GO:0006954; P:Inflammatory response; TAS. DR GO: GO:0009445; P:Pathogenesis; TAS. DR InterPro: IPR000276; GPCR_Rhodopsn. DR Pfam: PF00001; Tcm1_1. DR PRINTS: PR00237; GPCR_RHODOPSN. DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_1; DR G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis; KW Polymorphism; DOMAIN 1 16 EXTRACELLULAR (POTENTIAL). FT DOMAIN 17 38 1 (POTENTIAL). FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 55 74 2 (POTENTIAL). FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 92 113 3 (POTENTIAL). FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 134 155 4 (POTENTIAL). FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 185 205 5 (POTENTIAL). FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 234 254 6 (POTENTIAL). FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 277 295 7 (POTENTIAL). FT DOMAIN 297 342 CYTOPLASMIC (POTENTIAL). FT DISULFID 90 173 BY SIMILARITY. FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL). FT VARIANT 224 224 A->D (IN dbSNP: 5938). FT VARIANT 95 95 /FTID=VAR_011851. FT VARIANT 227 227 N->S (IN dbSNP: 5939). FT VARIANT 338 338 /FTID=VAR_011852. FT CONFLICT 28 28 1 -> P (IN REF. 6). FT CONFLICT 66 66 F -> L (IN REF. 6). FT CONFLICT 95 95 C -> R (IN REF. 6). FT CONFLICT 227 227 HR -> TG (IN REF. 4). FT CONFLICT 227 228 HR -> TT (IN REF. 6). FT CONFLICT 247 247 P -> A (IN REF. 6). FT CONFLICT 316 316 K -> N (IN REF. 5).

SQ SEQUENCE 342 AA; 39203 MW; 890073C9EBA79228 CRC64;

Query Match 22.2%; Score 394; DB 1; Length 342; Best Local Similarity 32.6%; Pred. No. 8e-21; Mismatches 134; Indels 26; Gaps 10; Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;

Qy 11 FGNTSLCTRDYKTTKTOVLPFLTYLFFVGLTINGLAKRNFQIR--SKSNFI-IFLRTNTV 67 Db 3 PHDSHMDSBPFYT-LFPIVYSSIFVLGVANGYVLMWPARLYPCCKFNEK1FEMVNLT 60

CC 68 ISDLIMITTPFKILSDALKTGPLRLTFVQCVTSVIFYFTMVISISPLGLITDRYQT 127 Db 61 MADMLFLITPLWLVYYQQGNWILPKELCNVAGCLLFINTYCSVAFLGIVTYNRFQAVT 120

Qy 128 RFPEKTSNPKNLGLAKLSTVW---AFMFLLSLPNMLTNRQPRDK--NYTKKCSFLK 179 Db 121 RIPIQAQNTRKRGISLSLVIAVGASYSFLIDS--TNTVPDSASGGNVTRC-FEH 176

Qy 180 SEFGLYWHIEWNYICQVIIWINFLIVYCYTLKELYKESTIWLTSINAICLDPPFYF 239 Db 177 YEKGSYPVLIHIFIYFSFLVFLILFNLVIRTLLMPVQQQRNAEVKEREALWM-VC 235

Qy 240 IIIAAYPPFCVPPHPFARIPTYLSQSTDYFDCTAENTLYKESTIWLTSINAICLDPPFYF 299 Db 236 TVLAFFIICFVPHHVQLWTLLAFL-QPQDSKEHQAINDAHQVTLCLLTSNCVLDPPVYC 294

Qy 300 FLCKSFN-----SLISMLKCPSNSAT 320 Db 295 FLTKCFERKHLTEKEYSMSRSARKCSRAATT 322

RESULT 12

PAFR_CAVPO STANDARD; PRT; 342 AA.

ID PAFR_CAVPO ID PAFR_CAVPO AC P21556; DT 01-MAY-1991 (Rel. 18, Created) DT 01-AUG-1991 (Rel. 19, Last sequence update) DT 01-OCT-1996 (Rel. 34, Last annotation update) DE Platelet activating factor receptor (PAF-R). GN PTAFR.

OS Cavia porcellus (Guinea pig). OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Metazoa; Metazo; N [1] RN RN SEQUENCE FROM N.A.

RC TISSUE=Lung; RX MEDLINE=91101726; PubMed=1846231; RX Honda Z.-I., Nakamura M., Miki I., Minami N., Watanabe T., Seyama Y., Okada H., Toh H., Ito K., Miyamoto T., Shimizu T.; RT "Cloning by functional expression of platelet-activating factor receptor from guinea-pig lung"; RL Nature 349:342-346 (1991).

-|- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-|- SUBCELLULAR LOCATION: Integral membrane protein.

-|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: X56736; CA40060_1; DR PIR: S13638; S13638; InterPro: IPR000276; GPCR_Rhodopsn. DR Pfam: PF00001; Tcm1_1. DR

PRINTS; PR00237; GPRORHODPSN. G PROTEIN RECEPTOR F1-1;
 DR PROSITE; PS00337; G PROTEIN RECEPTOR F1-2; 1;
 DR PROSITE; PS5C62; G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis; DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 17 38 1 (POTENTIAL).
 FT DOMAIN 39 54 CYTOSMERIC (POTENTIAL).
 FT TRANSMEM 55 74 2 (POTENTIAL).
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 92 113 3 (POTENTIAL).
 FT DOMAIN 114 135 4 (POTENTIAL).
 FT TRANSMEM 134 155 5 (POTENTIAL).
 FT DOMAIN 156 184 CYTOSMERIC (POTENTIAL).
 FT TRANSMEM 185 205 6 (POTENTIAL).
 FT DOMAIN 206 233 CYTOSMERIC (POTENTIAL).
 FT TRANSMEM 234 254 7 (POTENTIAL).
 FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 277 296 CYTOSMERIC (POTENTIAL).
 FT DOMAIN 297 342 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC) (POTENTIAL).
 FT DISULFID 169 169 BY SIMILARITY.
 SQ SEQUENCE 90 173 342 AA; B6413B2A5C87B175 CRC64;

Best Match Score 392; DB 1; Length 342;
 Best Local Similarity 30.7%; Pred. No. 1e-20;
 Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

Qy 20 DYKLTQVLFLPLLYTVLFFVGLITNGLAMRIFQFI--RSKSNNFI-IFLKNTVYSDLMIL 76
 Db 10 DSEFRYTLFLPVVSLVLIANGVLMVARYPSKRLNEIKIFMNLTADLPLIT 69
 Qy 77 FPFKEKLSDALGTGPRLTPVFCQTSVIFVFTMVISISIISFLGLITIDRYQKTTTRPKTSNPK 136
 Db 70 IPLWIVVYSNQGNNFLPKFLCNLGLCFLINTYCSVAFLGVITTYNRFAVKPIKTAQAT 129
 Qy 137 NLLGKILSTWIM---AFMFLSLPMLILNQPRDKVNVKCSFLKSEFG---LWHA 187
 Db 130 TRKGIALSLVTVIAVIAASFLYMDSTNVENKAGSNNTIC-FEYERGSKPKVLIH 188
 Qy 188 EIVNYICQVI-FWNFLIVITCYLTRELYRSVTRGVGVKPRKVNVKFEILLAVFP 246
 Db 189 ----ICIVYRFVFLIICFLNCLYIILRQPKQNAEV-RERBALWVCTLAQVFV 242
 Qy 247 ICVPDPFHAFRIPYTLQSQTDFDCATTNLFYRESTIWLTLNACLDPEFLCKSFR 306
 Db 243 ICVPDHMMVOLPWTIASEL-GWPSSNHQAINDAHQVTLCLLSNCVLDPVICFLTKER 301
 Qy 307 NSLISMVKCPNSATSLSDQRKKGDDGPNEETPM 342
 Db 302 KHLSEKLNNRNSQKCSRVTDTGEMAIPNHTPV 337

RESULT 13
 EB12 HUMAN STANDARD: PRT; 361 AA.
 AC P322759; Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE EBV-induced G protein-coupled receptor 2 (EB12).
 GN EB12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed:8383238;
 RX MEDLINE:91188173; Birkenbach M.P., Jøefferen K., Yalamanchili R.R., Lenoir G.M.,
 RA Kirke B.; "Epstein-Barr virus-induced genes: first lymphocyte-specific G

Query Match	20.6%	Score 367;	DB 1;	Length 345;
Best Local Similarity	29.0%	Pred. No.	6.1e-19;	
Matches	93;	Conservative	72;	Mismatches 134; Indels 22; Gaps 9;
Qy	1	MQAVDNTUSAQNTNLSCTRDXVQLFPLIYTVFFVGLITNGLAMRIFQIRSKSNFI	60	
Db	17	MEPNSTIGNNSNRSCTTENFK--REFPYTIVLYVIFIWGLANGNSIIVYPLPKYKRSKTSV	74	
Qy	61	-IFLKNTVISPLMLITFPFKI-----LSDAQLGTCPLRTFVQCVTSVIFYPTMMSISIP	114	
Db	75	NVPMNLNAISDILFLPTITLEPFRDYVLRGSNXIFGDTP---CRIMYSMSYVNMNSIYF	129	
Qy	115	IQLITIDRYQXTRPFKTSNPKNLIGAKILSVVIAWMFLSLPMMILTNRQPDRGNVK	174	
Db	130	LTVLSVTRFLATVHPPLRLHTTSIGNAWILQGVW-IFIMASSTVLLNGSEQDNVTI	187	
Qy	175	CSFLIKSEFGVWHEATVNYICCVI-FWNEFLIVIVCYTLKELYRSYVRTRGVGVKPRK	233	
Db	188	CLELNIN-KVTKLKMNVYVALVGGVLPFGLTISVLLI-TRALLKEVEPVPEGL-RUSHRK	245	
Qy	234	VNVKVELIIIAFFCIVPFHAPIPYTLSQTRDVSCTAENTLFYKESTIWLTSLNACI	293	
Db	246	ALITVITALIIFLFLCPFLPVHLRTLLEWKAD---KCDDRDLHKAVALTLLAAANSCP	301	
Qy	294	DPIFYFLCKSFRNSLJSMLK 314		
Db	302	NPFLYFAGENFKDRUKSALR 322		
RESULT 15				
PAFR_MOUSE				
ID	P-AFR_MOUSE	STANDARD;	PRT;	341 AA.
AC	Q62035;			
DT	15-JUL-1998	(Ref. 36, Created)		
DT	15-JUL-1998	(Ref. 36, Last sequence update)		
DT	15-JUL-1998	(Ref. 36, Last annotation update)		
DB	Platelet activating factor receptor (PAF-R).			
GN	PTAFR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
NCBI_TaxID	10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/Sv;			
RX	MEDLINE=96239129; PubMed=8670084;			
RA	Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T.,			
RA	Noma M., Shimizu T.;			
RT	"A murine platelet activating factor receptor gene: Cloning, chromosomal localization and up-regulation of expression by lipopolysaccharide in primary resident macrophages".			
RT	Biochem J 314: 671-678 (1996).			
RL				
CC	- - FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR. A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-			
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC	D50872; BAA03468_1; -			
CC	PIR: S63666; S63666.			
CC	DR: MGI:106056; Ptair.			
CC	InterPro: IPR000276; GPCR_Rhodopsin.			
CC	EMBL: D50872;			
CC	DR: PIR: S63666; S63666.			
CC	DR: MGI:106056; Ptair.			
CC	InterPro: IPR000276; GPCR_Rhodopsin.			

DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00337; G-PROTEIN RECEPTOR_F1-1; 1.
 DR PROSITE: PS00262; G-PROTEIN_BECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.

FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 17 38 1 (POTENTIAL).
 FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 74 2 (POTENTIAL).
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 92 113 3 (POTENTIAL).
 FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 4 (POTENTIAL).
 FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 5 (POTENTIAL).
 FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 234 254 6 (POTENTIAL).
 FT DOMAIN 255 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 295 7 (POTENTIAL).
 FT DOMAIN 296 341 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT DISULFID 90 173 BY SIMILARITY.

SEQUENCE 341 AA; 39148 MW; CAA8CDDDBD26897 CR64;
 SQ Score 20.6%; Score 366; DB 1; Length 341;
 Best Local Similarity 29.9%; Prd; No. 7; le-19;
 Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

Qy 20 DYKITQVLFFPLLYTVLFFVGLITNGLMRIFQI--RSKSNTI-IPIKNNTYSDLMILIT 76
 Db 10 DSEPRYTLPPVIVSVIPIVQVYVANGYVLLWVFVFLIGVYQVAVYPTIKTAQAT 69

Qy 77 FPFKFLDAKLGSPRLPTEVQOUTSVIIFYTMNISIPIGLITDQKTRPEFTSNPK 136
 Db 70 LPLWIVYYNEGDPWLNPFLCNVAGCLLFFINTYCSVAFLGVITNYQAVAYPTIKTAQAT 129

Qy 137 NLIGAKIISVVVIAFM---FELSLPMILTNRQPDDANVKCSFLRSBERG--LYWHE 188
 Db 130 TRKGISLSLIVVYKSYTATASTYLATDISTNLVNPNGSGNTTRCEHYEPYSVPLWVWV 189

Qy 189 IAVYICQVTFWVNFPLI-VIVCYTLLTKEVSYVTRGKVKVNVKFIIIAVFFI 247
 Db 190 FIAFCFLFVFLFYCNLVVHLLTQEMRQQ-RXRGV--KRRAWMVCTVLAVFII 243

Qy 248 CFYEPFHAFARIPTYLISQETDVFDCTAENTLFYKESTMLTSNACLDPEFYFLCKSFRN 307
 Db 244 CFYEPFHIVVQLPWTLAELG-YQTNFHQIANDAHQITULLSTNCVLDPVIVCFLTKKFRK 301

Qy 308 -----SLISMILKCPCNSATS 321
 Db 302 HLESEKFYSNRSSSRKC-SRATS 321

Search completed: February 4, 2004, 14:29:33
 Job time : 19 secs